

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 12:05:54 ; Search time 13.54 Seconds

(without alignments)
1286.839 Million cell updates/sec

Title: US-09-471-459A-5

Perfect score: 2408
Sequence: 1 MSLMVERCGEILFENPDQN.....PDHDAGGTESEEGDPS 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2408	100.0	450	1 CN7B_HUMAN	09np56 homo sapien
2	2192	91.0	446	1 CN7B_MOUSE	09q9x1 mus musculu
3	1425.5	59.2	456	1 CN7A_MOUSE	P70453 mus musculu
4	1419.5	58.9	482	1 CN7A_HUMAN	Q13946 homo sapien
5	1397.5	58.0	426	1 CN7A_RAT	008593 rattus norv
6	604.5	25.1	809	1 CNAD_HUMAN	008499 homo sapien
7	603.5	25.1	672	1 CNAD_RAT	P14270 rattus norv
8	580.5	24.1	721	1 CNAB_RAT	P14646 rattus norv
9	567.5	23.6	736	1 CNAB_HUMAN	Q07343 homo sapien
10	565	23.5	886	1 CNAA_HUMAN	P27615 homo sapien
11	559.5	23.2	610	1 CNM2_RAT	P14645 rattus norv
12	559.5	23.2	844	1 CNMA_RAT	P54748 rattus norv
13	553	23.0	712	1 CNMC_HUMAN	008493 homo sapien
14	529.5	22.0	536	1 CNMC_RAT	P14644 rattus norv
15	517	21.5	549	1 YST1_CAEEL	Q22000 caenorhabd
16	493	20.5	584	1 CNM1_DROME	P12352 drosophila
17	468	19.4	535	1 CNJB_MOUSE	001065 mus musculu
18	467	19.4	534	1 CNJB_BOVIN	001061 bos taurus
19	466	19.4	534	1 CNIA_HUMAN	P54750 homo sapien
20	466	19.4	535	1 CNIB_RAT	001066 rattus norv
21	466	19.4	565	1 CNIA_MOUSE	061481 mus musculu
22	461	19.1	664	1 YFGK_CAEEL	Q18696 caenorhabd
23	461	19.1	793	1 REGA_DICDI	Q23917 dictyostell
24	460	19.1	823	1 CNBA_MOUSE	008502 mus musculu
25	454.5	18.9	529	1 CNIA_BOVIN	P14100 bos taurus
26	452.5	18.8	768	1 CNIC_RAT	Q63421 rattus norv
27	450.5	18.7	654	1 CNIC_MOUSE	Q64338 mus musculu
28	449	18.6	536	1 CNIB_HUMAN	001064 homo sapien
29	448.5	18.6	709	1 CNIC_HUMAN	Q14123 homo sapien
30	445.5	18.5	713	1 CNBA_HUMAN	060658 homo sapien
31	441	18.3	659	1 CNBB_HUMAN	095263 homo sapien
32	422	17.5	534	1 CNNA_MOUSE	070628 mus musculu
33	399	16.6	593	1 CN9A_HUMAN	070683 homo sapien

34	381	15.8	875	1 CN5A_HUMAN	076074 homo sapien
35	378	15.7	865	1 CN5A_CANFA	077746 canis fam1
36	375	15.6	865	1 CN5B_BOVIN	Q28156 bos taurus
37	368.5	15.3	1112	1 CN5B_HUMAN	Q13370 homo sapien
38	362	15.0	833	1 CN5A_RAT	Q13370 rattus norv
39	357.5	14.8	1108	1 CN5B_RAT	Q54735 rattus norv
40	354	14.7	799	1 CN3B_MOUSE	Q61409 mus musculu
41	351	14.6	1141	1 CN3A_RAT	Q62865 rattus norv
42	346	14.4	1141	1 CN3A_HUMAN	Q14432 homo sapien
43	303.5	12.6	858	1 CNRC_HUMAN	P51160 homo sapien
44	300	12.5	855	1 CNRC_BOVIN	P15586 bos taurus
45	299	12.4	928	1 CN2A_RAT	Q01062 rattus norv

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	450 AA.
1	CN7B_HUMAN			
ID	CN7B_HUMAN			
AC	09np56:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).			
GN	PDE7B.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
NCBI	TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=20275458; PubMed=10814504;			
RA	Sasaki T., Kotera J., Yuasa K., Omori K.;			
RT	"Identification of human PDE7B, a CAMP-specific phosphodiesterase.";			
RL	Biochem. Biophys. Res. Commun. 271:575-583(2000).			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal brain;			
RX	MEDLINE=20329226; PubMed=10872825;			
RA	Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;			
RT	"Cloning and characterisation of the human and mouse PDE7B, a novel			
RL	CAMP-specific nucleotide phosphodiesterase.";			
CC	Biochem. Biophys. Res. Commun. 272:186-192(2000).			
CC	-1- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL			
CC	ACTIVITY AND CAMP METABOLISM IN THE BRAIN.			
CC	-1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =			
CC	ADENOSINE 5'-PHOSPHATE.			
CC	-1- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).			
CC	-1- ENZYME REGULATION: INHIBITED BY DIPYRIDADOLE, IBMX AND SCH51866.			
CC	INSENSITIVE TO ZAPRINAST, ROTIPRAM, AND MILRINONE.			
CC	-1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.			
CC	-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN. ALSO EXPRESSED IN			
CC	HEART, LIVER, SKELETAL MUSCLE AND PANCREAS.			
CC	-1- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO			
CC	PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.			
CC	-1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE			
CC	FAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
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CC	-----			
DR	EMBL: AB038040; BAA96537.1; -			
DR	EMBL: AJ251860; CAB92441.1; -			
DR	MM: 604645; -			
DR	InterPro: IPR003607; HDC.			
DR	InterPro: IPR002073; PDEase.			

DR Pfam: PF00233; PDBase: 1.
 DR PRINTS: PR00387; PDSTERASE1.
 DR SMART: SM00471; Hdc: 1.
 DR PROSITE: PS00126; PDBASE_I: 1.
 KW Hydrolase: CAMP.
 FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
 SQ SEQUENCE 450 AA; 51835 MW; EC142BF3E28D0028 CRC64;

Query Match 100.0%; Score 2408; DB 1; Length 450;
 Best Local Similarity 100.0%; Pred. No. 9.6e-188;
 Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSCIMVERGCEILFENPDONAKVCVMGDIRLGOTGVRAERGSYPFIDFLNSTYTS 60
 DB 1 MSCIMVERGCEILFENPDONAKVCVMGDIRLGOTGVRAERGSYPFIDFLNSTYTS 60
 QY 61 GEIGTKKKVRLSFORTFHASRLRGITIPAPLHLDEDDYLGOARHMLSKVGMDDPDTF 120
 DB 61 GEIGTKKKVRLSFORTFHASRLRGITIPAPLHLDEDDYLGOARHMLSKVGMDDPDTF 120
 QY 121 LFDRLTNGNSLVTLCHLFTNTHGLIHFKLDVTLHRELVYVQEDYHSONPYNNAVHAAD 180
 DB 121 LFDRLTNGNSLVTLCHLFTNTHGLIHFKLDVTLHRELVYVQEDYHSONPYNNAVHAAD 180
 QY 181 VTOAMHCYKLEPKLASFLTPDLIMGLAAAHVDHPGVNOPFLIKTNHNLANTYONMS 240
 DB 181 VTOAMHCYKLEPKLASFLTPDLIMGLAAAHVDHPGVNOPFLIKTNHNLANTYONMS 240
 QY 241 VLENHNRSTIGMLRESRLAHLPKEMTODIEOOLGSLIATDINRONEFLTRKAHLN 300
 DB 241 VLENHNRSTIGMLRESRLAHLPKEMTODIEOOLGSLIATDINRONEFLTRKAHLN 300
 QY 301 KDLRLDADDRHFMQIALKCADICNPCRIMWMSKOMSERVCEEFYRQGLBOKFELETS 360
 DB 301 KDLRLDADDRHFMQIALKCADICNPCRIMWMSKOMSERVCEEFYRQGLBOKFELETS 360
 QY 361 PLCNQOKDSIPSIQIGFMSYIVPLFRMAHFTGNSTLSENNLGHANAKQKSLPRQ 420
 DB 361 PLCNQOKDSIPSIQIGFMSYIVPLFRMAHFTGNSTLSENNLGHANAKQKSLPRQ 420
 QY 421 HRSRGSSGPDHHDAGGTSEEDGSDSP 450
 DB 421 HRSRGSSGPDHHDAGGTSEEDGSDSP 450

RESULT 2
 CN7B_MOUSE STANDARD: PRT: 446 AA.
 AC Q50XQ1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (BC 3.1.4.17).
 GN PDE7B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20087273; PubMed=10618442;
 RA Hettman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
 RT "Cloning and characterization of PDE7B, a CAMP-specific
 RT phosphodiesterase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C7BL/6J;
 RX MEDLINE=20329226; PubMed=10872825;
 RA Gardner C.E., Robas N.M., Cawkill D., Fildock M.D.;
 RT "Cloning and characterisation of the human and mouse PDE7B, a novel
 RT CAMP-specific nucleotide phosphodiesterase.";

RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL
 CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.
 CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
 CC ADENOSINE 5'-PHOSPHATE.
 CC -1- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
 CC -1- ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.
 CC -1- INSENSITIVE TO ZAPRINAST, ROLIPRAM, AND MLIRINONE.
 CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
 CC -1- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
 CC PUTATIVE DIVERGENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 CC FAMILY.
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 CC -----
 DR EMBL: AF190638; AAF25195.1; -
 DR EMBL: AJ251859; CAB92530.1; -
 DR MGI: MGI:1352752; Pde7b.
 DR InterPro: IPR003607; Hdc.
 DR InterPro: IPR002073; PDBase.
 DR Pfam: PF00233; PDBase: 1.
 DR PRINTS: PR00387; PDSTERASE1.
 DR SMART: SM00471; Hdc: 1.
 DR PROSITE: PS00126; PDBASE_I: 1.
 KW Hydrolase: CAMP.
 FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
 SQ SEQUENCE 446 AA; 51337 MW; 7C052664B593A5A8 CRC64;

Query Match 91.0%; Score 2192; DB 1; Length 446;
 Best Local Similarity 91.6%; Pred. No. 3e-170;
 Matches 413; Conservative 13; Mismatches 19; Indels 6; Gaps 2;

QY 1 MSCIMVERGCEILFENPDONAKVCVMGDIRLGOTGVRAERGSYPFIDFLNSTYTS 60
 DB 1 MSCIMVERGCEILFENPDONAKVCVMGDIRLGOTGVRAERGSYPFIDFLNSTYTS 60
 QY 61 GEIGTKKKVRLSFORTFHASRLRGITIPAPLHLDEDDYLGOARHMLSKVGMDDPDTF 120
 DB 61 GEIGTKKKVRLSFORTFHASRLRGITIPAPLHLDEDDYLGOARHMLSKVGMDDPDTF 120
 QY 121 LFDRLTNGNSLVTLCHLFTNTHGLIHFKLDVTLHRELVYVQEDYHSONPYNNAVHAAD 180
 DB 121 LFDRLTNGNSLVTLCHLFTNTHGLIHFKLDVTLHRELVYVQEDYHSONPYNNAVHAAD 180
 QY 181 VTOAMHCYKLEPKLASFLTPDLIMGLAAAHVDHPGVNOPFLIKTNHNLANTYONMS 240
 DB 181 VTOAMHCYKLEPKLASFLTPDLIMGLAAAHVDHPGVNOPFLIKTNHNLANTYONMS 240
 QY 241 VLENHNRSTIGMLRESRLAHLPKEMTODIEOOLGSLIATDINRONEFLTRKAHLN 300
 DB 241 VLENHNRSTIGMLRESRLAHLPKEMTODIEOOLGSLIATDINRONEFLTRKAHLN 300
 QY 301 KDLRLDADDRHFMQIALKCADICNPCRIMWMSKOMSERVCEEFYRQGLBOKFELETS 360
 DB 301 KDLRLDADDRHFMQIALKCADICNPCRIMWMSKOMSERVCEEFYRQGLBOKFELETS 360
 QY 361 PLCNQOKDSIPSIQIGFMSYIVPLFRMAHFTGNSTLSENNLGHANAKQKSLPRQ 420
 DB 361 PLCNQOKDSIPSIQIGFMSYIVPLFRMAHFTGNSTLSENNLGHANAKQKSLPRQ 420
 QY 421 HRSRGSSGPDHHDAGGTSEEDGSDSP 450
 DB 421 HRSRGSSGPDHHDAGGTSEEDGSDSP 450

Oy	127	NGSLVLTLLCGLNFTNFHLLHHFKLIDMTYLFRELYVMQEOYSQNPVHNNAVHAADVTQAMH	186
Oy	127	: : : : : : : : :	
Dd	140	NGNSLVSTFLEFLSHGELIEIFHLIDMKYKLRPLVMIOEDTHSQNPYHNNAVHAADVTQAMH	199
Oy	187	CYLEKEPKIASFLPFLDITMLIGLLAAAHADVDPGVNOFPFLKTNNHIANLYONMSYLENNH	246
Dd	200	CYLKEPKIASSVPFWMDILLSLIAAATGHDDHDHPGVNOPLIKTNHYLATLYLKSSVLENHH	259
Oy	247	WRSTITGMRSRLALPHKEMTDIEOQLSGSLIADDINRQNEFLTRLKAHLHKNDRLIE	306
Dd	260	MRSVAGLGIRESGFLSHLPESRKQEMEQAIALIADISKQNYLSLFRSHDKDGDLHND	319
Oy	307	DAORHFMLTALCALCAICNPCRTWEMSQKSECVCEEPFYROGELOKFELETISPCLNQ	366
Dd	320	DGRHRHLVALMALCAICAIQNCPCRWELSKMSKSVETEEFFHQSDIKKHLYGVSPLCDRQ	379
Oy	367	KDSIPSIQIGMFSYVEPLFREMAHFTGNSTLENNIGHLANHKAQWSILPRQHSRGS	426
Dd	380	TESTANIQIGMTVLVERPLTFENARFSA-TRLQSOTMLGHVKAKASKWGLOQRQSSEDA	438
Oy	427	SGS 429	
Dd	439	NAA 441	
RESULT 4			
ID	CNTA_HUMAN	STANDARD;	PRT; 482 AA.
AC	013946; 015380;		
DT	15-JUL-1998 (Rel. 36, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DE	16-OCT-2001 (Rel. 40, last annotation update)		
DE	High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A		
DE	(EC 3.1.4.11) (HCP1) (TM22).		
GN	PDE7A.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (PDE7A1).		
RA	MEDLINE=93286141; Pubmed=8389765;		
RX	Michaeli T., Bloom T.J., Martins T., Loughney K., Ferguson K.,		
RA	Riggs M., Rodgers L., Beavo J.A., Wiggler M.;		
RT	"Isolation and characterization of a previously undetected human cAMP		
RT	phosphodiesterase by complementation of cAMP phosphodiesterase-		
RL	deficient Saccharomyces cerevisiae.";		
RN	J. Biol. Chem. 268:12925-12932(1993).		
RN	[2]		
RP	SEQUENCE FROM N.A. (PDE7A2).		
RC	TISSUE=skeletal muscle;		
RX	MEDLINE=97341143; Pubmed=9195912;		
RA	Han P., Zhu X., Michaeli T.;		
RT	"Alternative splicing of the high affinity cAMP-specific		
RT	phosphodiesterase (PDE7A) mRNA in human skeletal muscle and heart.";		
RL	J. Biol. Chem. 272:16152-16157(1997).		
CC	-I- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE		
CC	INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS		
CC	PHOSPHODIESTERASE IS HIGHLY SPECIFIC FOR CAMP AND MAY HAVE A ROLE		
CC	IN MUSCLE SIGNAL TRANSDUCTION.		
CC	-I CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =		
CC	ADENOSINE 5'-PHOSPHATE.		
CC	-I COFACTOR: REQUIRES DIVALENT CATIONS.		
CC	-I ENZYME REGULATION: INSENSITIVE TO ALL SELECTIVE PDE INHIBITORS.		
CC	-I PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.		
CC	-I SUBCELLULAR LOCATION: PDE7A1 (57 kDa) IS LOCATED MOSTLY TO SOLUBLE		
CC	CELLULAR FRACTIONS. PDE7A2 (50 kDa) IS LOCATED TO PARTICULATE		
CC	CELLULAR FRACTIONS.		
CC	-I ALTERNATIVE PRODUCTS: 2 ISOFORMS: PDE7A1 (SHOWN HERE) AND PDE7A2;		
CC	ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER AT THEIR N-		
CC	TERMINAL REGION.		
CC	-I TISSUE SPECIFICITY: PDE7A1 IS FOUND AT HIGH LEVELS IN SKELETAL		

CC MUSCLE AND AT LOW LEVELS IN A VARIETY OF TISSUES INCLUDING BRAIN
 CC AND HEART. IT IS EXPRESSED AS WELL IN TWO T-CELL LINES. PDE7A2 IS
 CC FOUND ABUNDANTLY IN SKELETAL MUSCLE AND AT LOW LEVELS IN HEART.
 CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTALLY REGULATED. PDE7A1 AND -2 ARE
 CC FOUND IN SEVERAL FETAL TISSUES, EXPRESSION IS REDUCED THROUGHOUT
 CC DEVELOPMENT. IT PERSISTS STRONGLY ONLY IN ADULT SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
 CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 CC FAMILY.
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 CC -----
 CC EMBL: L12052; AAA35644.2; -
 CC EMBL: U67932; AAB65772.1; -
 CC MIM: 171885; -
 CC InterPro: IPR003607; HDC.
 CC InterPro: IPR002073; PDEase.
 CC Pfam: PF00233; PDEase; 1.
 CC SMART: SM00471; HDC; 1.
 CC DR PROSITE: PS00126; PDEASE_1; 1.
 CC DR HYDROLASE: CAMP; Phosphorylation: Alternative splicing.
 CC KM HYDROLASE: 28 33 POLY-SER.
 CC FT DOMAIN 187 451 CATALYTIC (BY SIMILARITY).
 CC FT MOD_RES 84 84 PHOSPHORYLATION (POTENTIAL).
 CC FT VARSPLIC 1 46 MEVCYOLPVLPDRPVPVLRGALISRGALISSSSSALFGCPNP
 CC ROLSO -> MGITLWICLALVLIKMTSK (IN ISOFORM
 CC PDE7A2).
 CC FT
 CC SEQUENCE 482 AA; 55505 MW; 3B3C8FEE9154F8BC CRC64;

Query Match 58.9%; Score 1419.5; DB 1; Length 482;
 Best Local Similarity 61.7%; Pred. No. 1,4e-107;
 Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

QY 7 ERCEGLFENPDONAKGCMIGDIRLGOTGVAERGSYPFLDPLNSTYSSGIGTK 66
 DB 46 QRGKISTDSDQFALYIRMGIDVRSRAGFESERGSHPYIDFLPHASQSIIEVSVA 105
 QY 67 KKKVRLSFOXYFHASRLRGILIPQAPLHLIDEDYLGOAARHMSKYGMDPDLFLDRLT 126
 DB 106 RIRRLSFOKRLNSRFRSTAVNSLNLLDDYNGQAKCMLEKVGNNMFDFLDRLT 165
 QY 127 NGNSLVTLCHLEFNTGHLIHFKLDVTLHRELVMVOEDYHSONPYHNAHADVTQAMH 186
 DB 166 NGNSLVSLTFHLFSLHGLEFPHIDMKLRFLVMIOEDYHSONPYHNAHADVTQAMH 225
 QY 187 CYLKEPKLASFLPLDLMGLLAAAHVDVPGVNOFELIKTHNLANTLYONKSVLENH 246
 DB 226 CYLKEPKLANSVTPMDILSLIAAATHDHPVNOFELIKTHNYLATYKNTSVLENH 285
 QY 247 WRSTIGMLRESRLAHLKPKENTODIEQGLSLIATDINRONFELTRLKAHLNKKDLRL 306
 DB 286 WRSVAVGLRESGLFSHPLRESROOEMTOIGALLIATDISRONYELSLFHSRDLGDLCE 345
 QY 307 DAORHFMLOALACADICNCPRIWMSKOMSERVCEEFROGELSEKFELEISPCNCO 366
 DB 346 DTRHRHVLQWALACADICNCPRIWMSKOMSERVCEEFROGELSEKFELEISPCNCO 405
 QY 367 KDSIPSTIOIGFMSYIVLEPFEAMHFTGNSISNNMGHLAHKAAKMSILPPIROHSRS 426
 DB 406 TESTANIOIGFMYIVLEPFEAMHFTGNSISNNMGHLAHKAAKMSILPPIROHSRS 464
 QY 427 SGS 429
 DB 465 DAA 467

RESULT 5
 ID CN7A_RAT STANDARD: PRT; 426 AA.
 AC 008593;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE High-affinity CAMP-specific 3',5'-cyclic phosphodiesterase 7A
 DE (EC 3.1.4.17) (Rolipram-insensitive phosphodiesterase type 7)
 DE (Fragment).
 GN PDE7A.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain.
 RX MEDLINE=98176136; PubMed=9515162;
 RA Hofmann R., Abdel'AI S., Engels P.;
 RT Differential distribution of rat PDE-7 mRNA in embryonic and adult
 RL rat brain.
 CC -1- Function: Biophys. 28:103-113(1998).
 CC INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
 CC PHOSPHODIESTERASE IS HIGHLY SPECIFIC FOR CAMP AND MAY HAVE A ROLE
 CC IN MUSCLE SIGNAL TRANSDUCTION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
 CC ADENOSINE 5'-PHOSPHATE.
 CC -1- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
 CC -1- ENZYME REGULATION: INSENSITIVE TO ALL SELECTIVE PDE INHIBITORS (BY
 CC SIMILARITY).
 CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
 CC -1- ALTERNATIVE PRODUCTS: THERE ARE DIFFERENT ISOFORMS PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
 CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U77880; AAB51234.1; -
 CC InterPro: IPR003607; HDC.
 CC InterPro: IPR002073; PDEase.
 CC Pfam: PF00233; PDEase; 1.
 CC SMART: SM00471; HDC; 1.
 CC DR PROSITE: PS00126; PDEASE_1; 1.
 CC KM HYDROLASE: CAMP; Alternative splicing.
 CC FT NON_TER 1 1
 CC FT DOMAIN 131 395 CATALYTIC (BY SIMILARITY).
 CC SEQUENCE 426 AA; 49274 MW; 129BDC01C9351D26 CRC64;

Query Match 58.0%; Score 1397.5; DB 1; Length 426;
 Best Local Similarity 62.4%; Pred. No. 6.9e-106;
 Matches 257; Conservative 68; Mismatches 86; Indels 1; Gaps 1;

QY 18 DONAKGCMIGDIRLGOTGVAERGSYPFLDPLNSTYSSGIGKKVRLSFSOR 77
 DB 1 DQFALYIRMGIDVRSRAGFESERGSHPYIDFLPHASQSIIEVSVAIRIRRLSFSOR 60
 QY 78 YFHASRLRGILIPQAPLHLIDEDYLGOAARHMSKYGMDPDLFLDRLTNGNSLVTLCH 137
 DB 61 YLRSRFRGATVCRSLNLLIDEDYNGQAKCMLEKVGNNMFDFLDRLTNGNSLVSLTFH 120


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Db 218 KEKKRPMQISGVKKLMHSSSLNCSIPRGVKTEDVDLAKE--LEDVKNKGLHVF 274
QY 122 FDRLLNGSLVTLTLLCH-LEFNHGLIHFKLMVTLHRLVAVQEDYHSQNPYNAVHAD 180
Db 275 IAEI-SCGRPLTLMHTFOERDLTKFKIPVDLTLYLMTLEHDVAVYHNHIAAD 333
QY 181 VTQAMHCYKPEKPLASFELTPDIMGLLAAAHVDHPGVQPEFLIKTNHNLANYOMNS 240
Db 334 VVQSTHVLSTPALLEAVTDEILAAITASAIIHDVHDGVSNOGLINTNSLALMYNDSS 393
QY 241 VLENHMHSTIGMLRESR-LLAHLPEKMTODIEQGLSLIADINRONEFLRLKAHL 298
Db 394 VLENHHLAVGFKLLQEEKNDIFOMLTKQROSLRKMADIYLAIDMSKHMMLADLKTMY 453
QY 299 HNKD-----LRDADDRHMLQIALKADICNCPKRWMSKSEVCEFTROGLE 352
Db 454 ETKKVTSSGVLLDNYSRIOVLQNMVHCADLSNPKLOLYRQWTDIMEEFPQDRE 513
QY 353 QKFELEISPLCNOQKDSIPSIQIFMSYIPELPFRENHFGNSTLSNNMLGHLAHNKAQ 412
Db 514 RERGMESIPMDKHNASVEKSOVGFIDYIVHPLMETWADLVHPD--KODIIDTLEDNRW 571
QY 413 WKSLLPQHRSRGSSGSPDHHDAGQTESE-----EQEGDS 449
Db 572 YQSTIPQ-----SPSPAPDDQEDGROQOTEKQFELTLEDGDS 610

RESULT 8
CNAB_RAT 8
ID CNAB_RAT STANDARD; PRT; 721 AA.
AC P14646;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CAMP-dependent 3',5'-cyclic phosphodiesterase 4B (EC 3.1.4.17)
DE (PDE4B).
GN PDE4B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A. (PDE4B3).
RA Huston E., Simon L., Annette R., Catterall C., Ross A.H., Steele M.R.,
RA Bolger G.B., Perry M., Owens R., Houslay M.D.,
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN 121
RP SEQUENCE OF 160-721 FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=89264471; Pubmed=2542941;
RA Colicelli J., Birchmeier C., Michaeli T., O'Neill K., Riggs M.,
RA Wiegler M.;
RT "Isolation and characterization of a mammalian gene encoding a high-
RT affinity CAMP phosphodiesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:3599-3603(1989).
RN 131
RP SEQUENCE OF 289-638 FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=89315790; Pubmed=2546153;
RA Swinnen J.V., Joseph D.R., Conli M.;
RT "Molecular cloning of rat homologues of the Drosophila melanogaster
RT dunce CAMP phosphodiesterase: evidence for a family of genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).
RN 141
RP SEQUENCE FROM N.A. (PDE4B2).
RX MEDLINE=95047482; Pubmed=7958996;
RA Bolger G.B., Rodgers L., Riggs M.;
RT "Differential CNS expression of alternative mRNA isoforms of the
RT mammalian genes encoding CAMP-specific phosphodiesterases.";
RL Gene 149:237-244(1994).
RN 151
RP SEQUENCE FROM N.A. (PDE4B2).

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RC STRAIN=WISTAR;
RX MEDLINE=94103234; Pubmed=8276818;
RA Monaco L., Vicini E., Conli M.;
RT "Structure of two rat genes coding for closely related rolipram-
RT sensitive CAMP phosphodiesterases. Multiple mRNA variants originate
RT from alternative splicing and multiple stat sites.";
RL J. Biol. Chem. 269:347-357(1994).
CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
CC ADENOSINE 5'-PHOSPHATE.
CC -1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; PDE4B1, PDE4B2 AND
CC PDE4B3 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U95748; AAB96560.1; -
DR EMBL; J04563; AAA66039.1; -
DR EMBL; M25350; AAA41846.1; -
DR EMBL; M28413; AAA41824.1; -
DR EMBL; L27058; AAA74478.1; -
DR EMBL; U01291; AAA18926.1; -
DR EMBL; U01289; AAA18926.1; JOINED.
DR EMBL; U01293; AAA18926.1; JOINED.
DR EMBL; U01294; AAA18926.1; JOINED.
DR EMBL; U01295; AAA18926.1; JOINED.
DR EMBL; U01296; AAA18926.1; JOINED.
DR EMBL; U01297; AAA18926.1; JOINED.
DR EMBL; U01298; AAA18926.1; JOINED.
DR EMBL; U01290; AAA18926.1; JOINED.
DR PTR; D33904; D33904.
DR InterPro: IPR003607; HDC.
DR InterPro: IPR002073; PDEase.
DR Pfam: PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CAMP; Alternative splicing; Multigene family.
FT VARSPPLIC 1 196
FT MTAKNSKKELEPASEEVCITFKQMKLELEPKLPGRPT
FT SPKISPRSSPNSPCFPKRLKLVNKSIRRRRTVAHCFDY
FT ENGPSGRSPLDQASSSGGLVLAAPFGHSGHRESEFLYS
FT DSDYDLSPKAMSRNSLPSBOHGDLDLVTFPAQVLAASRTY
FT RNNFTLTLNHLGAPNKRSPPAASQAPVTRVSLQ -> MKEGG
FT CTVSGAGSSSRGGGDSMAAISQPLQPNLTSLCLFA (IN
FT ISOFORM PDE4B2).
FT T -> S (IN REF. 5).
FT CONFLICT 516 516
FT SQ SEQUENCE 721 AA; 82100 MW; C6FB885B6107BDAD CRC64;

Query Match 24.1%; Score 580.5; DB 1; Length 721;
Best Local Similarity 31.9%; Pred. No. 2.3e-39;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

QY 66 KKKYKRLS-----FQRYFNASRLRGILPQAPRLHLDDEDYQGAQRHMLSKYGMDFDPL 121
Db 283 KKKKQQLMTQISGVKKLMHSSSLNNTSISRGVNTENDHLAKLEDLNK---WGLNIFN 339
QY 122 FDRLLNGSLVTLTLLCHLEFNHGLIHFKLMVTLHRLVAVQEDYHSQNPYNAVHADV 181
Db 340 VAGSHNPLTLCIMAIWFOERDLTKFKISSDFTVTYMTLEHDYHSDVAVYHNHIAADV 399
QY 182 TQAMHCYKPEKPLASFELTPDIMGLLAAAHVDHPGVQPEFLIKTNHNLANYOMNSV 241
Db 400 AOSTHVLSTPALDAVFTDEILAAITASAIIHDVHDGVSNOGLINTNSLALMYNDESV 459

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QY 242 LENHMRSTIGMLRESR--LAAHLPEKMTODIEQOLGSLIATDINFEKTRAKHL 299
DB 460 LENHHLAVGFKLQEEHCDFONLTKKORQTLRKAVYIDMVLATDMSKMSLADLKTIVE 519
QY 300 NKD-----LRLDAODRHFMLQIALKADICNPRIMEKSKNSERVICEEFTYQGELEQ 353
DB 520 TKRYTSSGVLLDNDYDRIOVLNRNVHCADLSNPKRSLRYRQMTDRIMEEFTYQGELEQ 579
QY 354 KFELEISPLCNOCKDSIPSIQIGFMSYIYELFREMAHFTGNSLSENMLGHLAANKAOW 413
DB 580 ERMEISLSPCKDKHTTASVKSQVGFIDYIYHPLMETMALDLYOPD--ADDIIDLTELDNNWY 637
QY 414 KSLLP-----OHRSGSSGSGPDDH---AGGTSESEDEQDSP 450
DB 638 QSMIPSPSPPLDERSRDCOGIMEKFOFELTLEEDSESGPERKEGCP 684

RESULT 9
CNAB_HUMAN STANDARD; PRT; 736 AA.
AC 007343; 015443;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE cAMP-dependent 3',5'-cyclic phosphodiesterase 4B (EC 3.1.4.17)
DE (PDE4B) (PDE32).
GN PDE4B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A. (PDE4B1 AND PDE4B2).
RC TISSUE=Brain;
RX MEDLINE=94019330; PubMed=8413254;
RA Bolger G., Michael T., Martins T., St John T., Steiner B.,
RA Rodgers L., Riggs M., Wigler M., Ferguson K.;
RT "A family of human phosphodiesterases homologous to the duncce
RT learning and memory gene product of Drosophila melanogaster are
RT potential targets for antidepressant drugs.";
RL Mol. Cell. Biol. 13:6558-6571(1993).
RN [2]
RP SEQUENCE FROM N.A. (PDE4B3).
RX MEDLINE=98041898; PubMed=9371714;
RA Huston E., Lumb S., Russell A., Catterall C., Ross A.H., Steele M.R.,
RA Bolger G.B., Perry M.J., Owens R.J., Houslay M.D.;
RT "Molecular cloning and transient expression in COS7 cells of a novel
RT human PDE4B cAMP-specific phosphodiesterase, HSPDE4B3.";
RL Biochem. J. 328:549-558(1997).
RN [3]
RP SEQUENCE FROM N.A. (PDE4B2).
RC TISSUE=Brain;
RX MEDLINE=93203241; PubMed=8384210;
RA McLaughlin M.M., Cieslinski L.B., Burman M., Torphy T.J.,
RA Livi G.P.;
RT "A low-Km, rolipram-sensitive, cAMP-specific phosphodiesterase from
RT human brain. Cloning and expression of cDNA, biochemical
RT characterization of recombinant protein, and tissue distribution of
RT mRNA.";
RL J. Biol. Chem. 268:6470-6476(1993).
CC -1- FUNCTION: MAY BE INVOLVED IN MEDIATING CENTRAL NERVOUS SYSTEM
CC EFFECTS OF THERAPEUTIC AGENTS RANGING FROM ANTIDEPRESSANTS TO
CC ANTIASTHMATIC AND ANTI-INFLAMMATORY AGENTS.
CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
CC ADENOSINE 5'-PHOSPHATE.
CC -1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS: PDE4B1 (SHOWN HERE),
CC PDE4B2 AND PDE4B3; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, LUNG AND SKELETAL
CC MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.

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CC or send an email to license@sib-sib.ch).
CC -----
DB EMBL; L20966; AAA03589.1; -
DB EMBL; L20971; AAA03593.1; -
DB EMBL; M97515; AAA36426.1; -
DB EMBL; U85048; AAB96381.1; -
DB MIM; 600127; -
DB InterPro; IPR003607; HDC.
DB InterPro; IPR002073; PDEase.
DB Pfam; PF00233; PDEase; 1.
DB PRINTS; PRO0387; PDIESTERASE1.
DB SMART; SM00471; HDC; 1.
DB PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CAMP; Alternative splicing: Multigene family.
VARSPPLIC 1 93 MKRSRYMTVMADNDVKKYFRCSLKSYSSSSNTIGDLMR
GRRCSGNLOLPISORSEKAPRPEDGTSRPTLPPLTL
PSIATTVYSOECEVDENSPGSRPRLDPOSSAGLVHAT
PPGHSQRRESPLVNSDDYDLSFPAKRNSSLSEGHQDL
IVTPPAOVLASLRSVRNNTLTLLNHTGTSKRKPASOPV
SRVNPQ -> MKKEHGTFSSGTIGSGSGSANDSTLOPLQ
NYMPVCLPA (IN ISOFORM PDE4B2).
SQ SEQUENCE 736 AA; 83343 MW; 208FCB9CD40EF5EB CRC64;
QY 66 KKKYKRLS---FORFYHNSRLRGITPOADPLHLDDEYDGAOAHNLSKVGMDPPIFL 121
DB 298 KKKKQOLMTQISGVKKMKHSSSLNNTSISRPOVNTENNEDHLAKELDNLK---WGLNIFN 354
QY 122 FDRLTNGNSVYTLCHFNHGLIHFKDYMVTLRPLVMOEDVHSGNPRYNAVHADV 181
DB 355 VAGSIHNRPLTCLYATFOERDLTKFRISDFTTYMTLEDNHSVAYHNSLHADV 414
QY 182 TQAHCTYKKEPKLASFLTPLDIMLGILAAADVDHGVNOFPDLIKTNHILANIYONKSY 241
DB 415 AOSTHVLSTPDLDAVFTDTEILATFAAHIDVHPGVSNOFLNTNSETALMYNDESV 474
QY 242 LENHMRSTIGMLRESR--LAAHLPEKMTODIEQOLGSLIATDINFEKTRAKHL 299
DB 475 LENHHLAVGFKLQEEHCDFONLTKKORQTLRKAVYIDMVLATDMSKMSLADLKTIVE 519
QY 300 NKD-----LRLDAODRHFMLQIALKADICNPRIMEKSKNSERVICEEFTYQGELEQ 353
DB 535 TKRYTSSGVLLDNDYDRIOVLNRNVHCADLSNPKRSLRYRQMTDRIMEEFTYQGELEQ 579
QY 354 KFELEISPLCNOCKDSIPSIQIGFMSYIYELFREMAHFTGNSLSENMLGHLAANKAOW 413
DB 595 ERMEISLSPCKDKHTTASVKSQVGFIDYIYHPLMETMALDLYOPD--ADDIIDLTELDNNWY 632
QY 414 KSLLP-----OHRSGSSGSGPDDH---AGGTSESEDEQDSP 448
DB 653 QSMIP-----SPSPPLDEONRDCOGIMEKFOFELTLEEDSESGPERKEG 697

RESULT 10
CN4A_HUMAN STANDARD; PRT; 886 AA.
AC P27815; Q16691; Q16255; Q75522; Q76092;

```


CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O -
CC ADENOSINE 5'-PHOSPHATE.
CC -1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF THE PROTEIN (PDE4C1 TO
CC PDE4C7) ARE PRODUCED BY ALTERNATIVE SPLICING. THE ISOFORM SHOWN
CC HERE IS PDE4C1.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES BUT NOT IN CELLS
CC OF THE IMMUNE SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: 246632; CAA86601.1; -
CC EMBL: L20968; AAA03591.1; -
CC MIM: 600128; -
CC DR InterPro: IPR003607; PDC.
CC DR InterPro: IPR002073; PDCase.
CC DR Pfam: PF00233; PDCase; 1.
CC DR PRINTS: PR00387; PDSESTRASE1.
CC DR SMART: SM00471; HDC; 1.
CC DR PROSITE: PS00126; PDCASE_I; 1.
CC DR HydroLase; CAMP, Multigene family; Alternative splicing.
CC SQ SEQUENCE: 712 AA; 79845 MW; 0EC70E917A393F78 CRC64;

Query Match 23.0%; Score 553; DB 1; Length 712;
Best Local Similarity 27.8%; Pred. No. 3.8e-37;
Matches 135; Conservative 94; Mismatches 158; Indels 58; Gaps 10;

OY 11 ELIFENDONAKCVMGDIRLGQGYAERGSYPIDRELLN-----STTYSG- 61
DB 204 KLALETLDELWCLDLETLQTRHSVGEMASNFK-----RIINRELTHLSETRSGNQ 257
OY 62 -----EIGTKK-----KVKRLSFQRYFASRLNGIIPQAPVHLHLE 99
DB 258 VSEYISRTFLDQOTEVELPKYAEBAPOPMRSISGLHGLCHSASLSATVPREGVOTDOE 317
OY 100 DYLGQARHMLSKVGMDFPIFLFDRLTNGNSLVTLTCLHFTNHLGHNFKIDVYTLHRL 159
DB 318 EQLAKE--LEDTNKMGDLDFKVAADVSGNRPFLTAIFISFQERDLMTFQIPADTLATYL 374
OY 160 VMVOEDYHSQNPYHNNAVHADYTOAMHCYLKEPKLASFLPLDITMIGLAAAHVDVHPG 219
DB 375 LMEGHYHNNAVYHNSIHADYVOSTHYLLATPRALEAVFTDLELALFSAIHVDVHPG 434
OY 220 VNPEPLIKNNHNLAYOMSYLENHNRSTIGMLRESR--LNAHLKREMTQDIEOOLGS 277
DB 435 VSNQFLITNSDVALMTNDASVLENHNLAVGFKLQAEKCDIFONLSAKORLSRRVAD 494
OY 278 LLIATDINONEFLTRKALHNKD-----LLEDAADRHEMLQIALKACADICNCRW 331
DB 495 MVLATMSKHMNLADLKMTVETKRVTSIGVLLDNYSDRTOVLQNVHCAADLSNPKPL 554
OY 332 EMKQSERVCEFFYKQGLPELLEISPLCNOOKDISPISQIFGFSYVEPLFRMAH 391
DB 555 PLRYQWTDRIIMAEFFQOGRERESGLDISPMCKHTASVEKSGYGFIDYIAHPLMETWAD 614
OY 392 FTGNSTLSNNMLGHLAHNKAQWKSLLPQOHS-RGSSSGSGDH-----DHAGQGGESE 443
DB 615 LVHPD--AODLDTLEDNREMYQSKIPRSPDLTPNRPDGRDROFETLLEAEEDDEE 672
OY 444 EOEGD 448
DB 673 EEEGE 677

RESULT 14
CNC_C_RAT STANDARD; PRT; 536 AA.
ID CNC_C_RAT
AC P1644;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CAMP-dependent 3',5'-cyclic phosphodiesterase 4C (EC 3.1.4.17)
DE (DDE1) (Fragment).
GN PDE4C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95047482; Pubmed-7958996;
RA Bolger G.B., Rodgers L., Riggs M.;
RT "Differential CNS expression of alternative mRNA isoforms of the
RT mammalian genes encoding CAMP-specific phosphodiesterases.";
RL Gene 149:237-244(1994).
RN [2]
RP SEQUENCE OF 153-511 FROM N.A.
RC TISSUE-Testis;
RX MEDLINE-89315790; Pubmed-2546153;
RA Swinnen J.V., Joseph D.R., Conzel M.;
RT Molecular cloning of rat homologues of the Drosophila melanogaster
RT dunce CAMP phosphodiesterase: evidence for a family of genes.
RL Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).
CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O -
CC ADENOSINE 5'-PHOSPHATE.
CC -1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC
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CC
CC EMBL: L27061; AAA56858.1; -
CC EMBL: M25347; AAA41847.1; -
CC PIR: A33904; A33904.
CC DR InterPro: IPR003607; HDC.
CC DR InterPro: IPR002073; PDCase.
CC DR Pfam: PF00233; PDCase; 1.
CC DR SMART: SM00471; HDC; 1.
CC DR PROSITE: PS00126; PDCASE_I; 1.
CC DR HydroLase; CAMP, Multigene family.
CC KW NON-TER
FT DOMAIN 524 534 POLY-GLU.
FT CONFLICT 218 218 R -> S (IN REF. 2).
FT CONFLICT 507 507 S -> N (IN REF. 2).
SO SEQUENCE 536 AA; 60063 MW; 87D12BE2C46642F3 CRC64;

Query Match 22.0%; Score 529.5; DB 1; Length 536;
Best Local Similarity 30.8%; Pred. No. 2.1e-35;
Matches 120; Conservative 79; Mismatches 169; Indels 21; Gaps 7;

OY 71 RLTSFYRYPASRLRRIIPQAPVHLHLEDDYLGQARHMLSKVGMDFPIFLFDRLTNGNS 130
DB 156 QITGLRKSCHTS-LPRAALIRPFGVGTDOEQLAKE--LEDTNKMGDLDFKVAELSGNRP 211
OY 131 LVTLTCLHFTNHLGHNFKIDVYTLHRLVMVOEDYHSQNPYHNNAVHADYTOAMHCYLK 190
DB 212 LTAIVIFRVLQERDLTKTFQIPADTLRLRYLTLEGRHNSVNAVHNSIHADYVQSAHYLLG 271

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RESULT 15
YSTL_CAEEL
ID YSTL_CAEEL STANDARD; PRT; 549 AA.
AC Q22000;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Probable 3',5'-cyclic phosphodiesterase R153.1 (EC 3.1.4.17).
GN R153.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Kirsten J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1 CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H2O =
CC nucleoside 5'-phosphate.
CC -1 SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY. STRONG, TO MAMMALIAN TYPE 4 CAMP PHOSPHODIESTERASES.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U28729; AAA68392.1; -.
DR WormPeep; R153.1; CE02038.
DR InterPro; IPR003607; HDC.
DR InterPro; IPR002073; PDbase.
DR Pfam; PF00233; PDbase; 1.
DR PRINTS; PRO0387; PD1ESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDbase_1; 1.
DR Hypothetical protein; Hydrolase; CAMP.
KW SEQUENCE 549 AA; 62904 MW; DF2EE6F03925DE87 CRC64;

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Query Match	21.5%;	Score 517;	DB 1;	Length 549;
Best Local Similarity	32.6%;	Pred. No. 2.2e-34;		
Matches 114;	Conservative 72;	Mismatches 140;	Indels 24;	Gaps 6

[illegible]

Db	275	HYRN-NHYNH-ITHAADVAQSMHVLMSVLTLEVYTTDEVLAIATAGAVHDVHGFTNQ	3333
QY	225	LKTHNHLANTYONKSMYENHHNSTGIMLEBSR-LLAHFKMTODIEQOSLILAT	282
Db	334	LINSNNEIATMYNDESYLEQHLLVAFELLLDSDSCDFLANISRRQLOFRYIDVYLAT	3939
QY	283	DINRONEFLTLKALHL-----NKDLRELEAOQRHMFALTKACADICNFCRIWESKO	3366
Db	394	DMSKMSLLADLKITVEAKKVAAGNNVILYLDKYNKIOVLQSMIHADLSNPTKRIELYQ	4534
QY	337	MSERCFEEFYRGOGELOKFEELTEIPLCIOQKDSIPISIOIGMSVYTBPLREMAHFGNS	3966
Db	444	MNQRIMEEYKQDKERKGLGIEIPMCDRGVNTLEKQSGVYDITVNPRLYETNADLYPD	5133
QY	397	TLSENMLCHLANHKAQWKSLLPROHRSKSGSGCPDHHDHAGOGTESEBOE	446
Db	514	-AQNIILOLEENREMYQSRPE-----EPATATYEDDEHK	549

Search completed: September 13, 2002, 12:10:05
Job time: 251 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 12:01:39 : Search time 16.3 Seconds
(without alignments)
674.326 Million cell updates/sec

Title: US-09-471-459A-5
Perfect score: 2408
Sequence: 1 MSCILVERKCEILEFNPDPN.....PDHHDAGCGTESEEGEDSP 450

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
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2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCOTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2258	93.8%	502	US-09-330-970-1	Sequence 1, App11
2	1419.5	58.9	498	US-07-688-352C-20	Sequence 20, App1
3	1419.5	58.9	498	US-08-474-379C-20	Sequence 20, App1
4	1419.5	58.9	498	US-09-146-249A-20	Sequence 20, App1
5	1419.5	58.9	498	US-08-206-188B-20	Sequence 20, App1
6	1280	53.2	320	US-09-330-970-3	Sequence 3, App11
7	604.5	25.1	673	US-08-474-379C-63	Sequence 63, App1
8	604.5	25.1	673	US-09-146-249A-63	Sequence 63, App1
9	599.5	24.9	673	US-08-206-188B-63	Sequence 63, App1
10	599.5	24.9	673	US-08-577-492-35	Sequence 35, App1
11	599.5	24.9	673	US-09-079-630-35	Sequence 35, App1
12	580.5	24.1	562	US-07-688-352C-4	Sequence 4, App11
13	580.5	24.1	562	US-08-942-521B-8	Sequence 8, App11
14	580.5	24.1	562	US-08-474-379C-4	Sequence 4, App11
15	580.5	24.1	562	US-09-146-249A-4	Sequence 4, App11
16	580.5	24.1	562	US-08-206-188B-4	Sequence 4, App11
17	580.5	24.1	562	PCT-US91-02714-4	Sequence 4, App11
18	567.5	23.6	564	US-08-577-492-34	Sequence 34, App1
19	567.5	23.6	564	US-08-942-521B-2	Sequence 2, App11
20	567.5	23.6	564	US-08-474-379C-59	Sequence 59, App1
21	567.5	23.6	564	US-09-146-249A-59	Sequence 59, App1
22	567.5	23.6	564	US-08-206-188B-59	Sequence 59, App1
23	567.5	23.6	564	US-09-192-702-2	Sequence 2, App11
24	567.5	23.6	564	US-09-079-630-34	Sequence 34, App1
25	567.5	23.6	564	US-08-445-474-2	Sequence 2, App11
26	567.5	23.6	564	PCT-US94-02612-2	Sequence 2, App11
27	567.5	23.6	736	US-07-688-352C-24	Sequence 24, App1

28	567.5	23.6	736	US-08-474-379C-24	Sequence 24, App1
29	567.5	23.6	736	US-09-146-249A-24	Sequence 24, App1
30	567.5	23.6	736	US-08-206-188B-24	Sequence 24, App1
31	567.5	23.6	736	PCT-US91-02714-23	Sequence 23, App1
32	565	23.5	885	US-08-577-492-33	Sequence 33, App1
33	565	23.5	885	US-09-079-630-33	Sequence 33, App1
34	565	23.5	886	US-08-474-379C-65	Sequence 65, App1
35	565	23.5	886	US-09-146-249A-65	Sequence 65, App1
36	565	23.5	886	US-08-206-188B-65	Sequence 65, App1
37	563	23.4	666	US-08-942-521B-9	Sequence 9, App11
38	562	23.3	606	US-08-577-492-32	Sequence 32, App1
39	562	23.3	606	US-09-079-630-32	Sequence 32, App1
40	560.5	23.3	404	US-08-474-379C-44	Sequence 44, App1
41	560.5	23.3	404	US-09-146-249A-44	Sequence 44, App1
42	560.5	23.3	404	US-08-206-188B-44	Sequence 44, App1
43	559.5	23.2	610	US-08-974-565C-9	Sequence 9, App11
44	559.5	23.2	610	US-09-255-748-9	Sequence 9, App11
45	558.5	23.2	481	US-08-286-856C-2	Sequence 2, App11

ALIGNMENTS

RESULT 1	US-09-330-970-1	Sequence 1, Application US/09330970
Patent No. 6146876		
GENERAL INFORMATION:		
APPLICANT: Robison, Keith E.		
APPLICANT: Kapeller-Libermann, Rosana		
APPLICANT: White, David		
TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide		
TITLE OF INVENTION: Phosphodiesterase		
FILE REFERENCE: 5800-28		
CURRENT APPLICATION NUMBER: US/09/330,970		
CURRENT FILING DATE: 1999-06-11		
EARLIER APPLICATION NUMBER: 09/277,423		
EARLIER FILING DATE: 1999-03-26		
NUMBER OF SEQ. ID NOS.: 40		
SOFTWARE: FASTSEQ for Windows Version 3.0		
SEQ. ID NO. 1		
LENGTH: 502		
TYPE: PRT		
ORGANISM: Homo sapiens		
US-09-330-970-1		
Query Match	93.8%	Score 2258; DB 4; Length 502;
Best Local Similarity	100.0%	Pred. No. 9.8e-229;
Matches 423; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	28	GDRLRGQTVRAERKSGYFIDRLINSTTYSGETGKTKKVKRLSFQRYFNASRLRG 87
DB	80	GDRLRGQTVRAERKSGYFIDRLINSTTYSGETGKTKKVKRLSFQRYFNASRLRG 139
QY	88	IIFQAPRLHLDDEYLGARHMLSKVGWMDPDLFQDLTGNSLVTLCHLFTNHGILHH 147
DB	140	IIFQAPRLHLDDEYLGARHMLSKVGWMDPDLFQDLTGNSLVTLCHLFTNHGILHH 199
QY	148	FKLDNVLHFLVWQEDYHSQNPYHNAVADVTQAMHCYLEKPKLASFLPLDITMGL 207
DB	200	FKLDNVLHFLVWQEDYHSQNPYHNAVADVTQAMHCYLEKPKLASFLPLDITMGL 259
QY	208	LAAAHVDHVPVNOPLITNNHNLAYONMSVLENHNRSTIGMLRESRLAHLPEKM 267
DB	260	LAAAHVDHVPVNOPLITNNHNLAYONMSVLENHNRSTIGMLRESRLAHLPEKM 319
QY	268	TDIEQGLSLIATDINRQNEFLTRKAHLHKKDLLEQADQDRHFMLOIALCADIQNP 327
DB	320	TDIEQGLSLIATDINRQNEFLTRKAHLHKKDLLEQADQDRHFMLOIALCADIQNP 379
QY	328	CRWEMSKQSEVCEEFYRQGELEQFELEISPLCNOQKDSIPSIOIGFMSYIVEPLFR 387

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Page 2

Db 380 CWMWSEKQSRVCEEFYRGELEFQFELEISPLCNOOKDIPSIOIGEMSYIEPLR 439
QY 388 EWAHTGNSSTLSENNLGHLANHKAOMKSLPROHRSRGSSGSPDDHAGOGTESEORG 447
Db 440 EWAHTGNSSTLSENNLGHLANHKAOMKSLPROHRSRGSSGSPDDHAGOGTESEORG 499
QY 448 DSP 450
Db 500 DSP 502

RESULT 2
US-07-688-352C-20
Sequence 20, Application US/07688352C
Patent No. 5527896
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,352C
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 964-5740
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-688-352C-20

Query Match 58.9% Score 1419.5 DB 1: Length 498;
Best Local Similarity 61.7% Pred. No. 1.3e-140;
Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

QY 7 ERGGILFENPDONAKCYMGLDRLRGOTGVAAERGGSPFIDFLINSTYSGEIGTK 66
Db 62 ORRGATISDSSDQALYVLMGIDVVRVSRAGFESERGGSPYIDFRIHFSQSEIEVSVA 121
QY 67 KKKVRLSFGYRFAHSLRLGIIIDAPLHLIDEDYLGQARHMLSKVGMDFIDFLRLT 126
Db 122 NRIIRLISFGYRFAHSLRLGIIIDAPLHLIDEDYLGQARHMLSKVGMDFIDFLRLT 181
QY 127 NNSLVTLCHLFTNGLIHFFKIDMYTLHRLFLVMVOEDHVSQNPYHNAVHADYQAAH 186

Db 182 NNSLVTLCHLFTNGLIHFFKIDMYTLHRLFLVMVOEDHVSQNPYHNAVHADYQAAH 241
QY 187 CYLKEPKLASFTLPDIDMIGLLAAAHVDHPGVNOPELITNHLNLYONNSVLENH 246
Db 242 CYLKEPKLASFTLPDIDMIGLLAAAHVDHPGVNOPELITNHLNLYONNSVLENH 301
QY 247 WRSTIGMLRESRLAHLPEKMTODIEQOGLIATDINRONEFLTRKAHLNKLRL 306
Db 302 WRSAVGLRESGLFSLPLESRQOMETOIGALIIATDISRONEFLTRSHLDIGDICLE 361
QY 307 DAQDRHFMLOIALKCADICNPICRIMEMSKOMSERVCEEFYRGELEFQFELEISPLCNOO 366
Db 362 DTRHRLHYLOMALKCADICNPICRIMEMSKOMSERVCEEFYRGELEFQFELEISPLCNOO 421
QY 367 KDSIPSTOIGFMSYIYEPFREMAGFTGNSLSENNLGHLANHKAOMKSLPROHRSRG 426
Db 422 TESTANIGQFMYLVEPFTEMARFS-NTRLSTGMLGHVGLNKAOMKSLPROHRSRG 480
QY 427 SGS 429
Db 481 DAA 483

RESULT 3
US-08-474-379C-20
Sequence 20, Application US/08474379C
Patent No. 5977305
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990

APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-379C-20

Mon Sep 16 16:41:06 2002

us-09-471-459a-5.rai

Page 4

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? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/511,715
? FILING DATE: 20-APR-1990
? ATTORNEY/AGENT INFORMATION:
? NAME: Clough, David W.
? REGISTRATION NUMBER: 36107
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312/474-6300
? TELEFAX: 312/474-0448
? TELEX: 25-3856
? INFORMATION FOR SEQ. ID NO.: 20:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 498 amino acids
? type: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-206-188b-20

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-379C-63

Query Match 25.1%; Score 604.5; DB 2; Length 673;
Best Local Similarity 33.3%; Pred. No. 9,9e-55;
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

QY 66 KKKVKRLS----FQRYFNASRLRGITPOAPRLHLLDEDTLGOARHMLSKVGMDFDIFL 121
DB 218 KKKKKRPMQISGVKKLMHSSSLTNSIPRGVKTQEDVLAKE--LEDVNMKGHLAVR 274
QY 122 FDRLTNGSLVTLTLC-LFNTHGLIHFKLDVTLHRLVLMVOEDYHSQNPYNNAAVHAD 180
DB 275 IAEI-SGNRPFLVIMHTIFQERDLTFKIPVDTLITLTLEDYHADVAANNHHAAD 333
QY 181 VTQAMHCYKEPKLASFLPLDMLGLAAAHADVDPGVNOPLFKTNHNLNLYQNM 240
DB 334 VQSTHVLSTPLAEVFDLELAIFASAIHDVDPGVSNQFLINTSELAAMYNDSS 393
QY 241 VLENHNRSTIGMLRESR--LNAHLPKEMTQDIEQOLGSLIATDINRONEFLTRKAL 298
DB 394 VLENHNLAVGFKLQENCDIFQNLTKKORSLRKAVIDIVLATDMSKHNMLADLKTW 453
QY 299 HNMD-----LRLEDADRHFMLOIALKCADICNPCRIMESKOMSERVCEERYGELE 352
DB 454 ETKKVTSSGVLLDNYSRQYVLQNNVHCADLSNPKPLQYKQMDRIIMEEFFRGDRE 513
QY 353 QKFELEISPLCNOOKDSIPSIQIGFMSYIPEPLRFREMAHFTGNSLSENNLGHANHAQ 412
DB 514 RERGMEISPMCKHNASVERKSGVGFIDYIVHPLMETWADLVHPD--AQDILDTLEDNREW 571
QY 413 WKSLPQRHRSRSGSGGPDHAGGTSE-----EQEGDS 449
DB 572 YOSTIPQ-----SPSPAPDDPEEGOGOTEKFOFELTLEEDGS 610

RESULT 8
US-09-146-249A-63
Sequence 63, Application US/09146249A
Patent No. 6069240
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715

FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-146-249A-63

Query Match 25.1%; Score 604.5; DB 3; Length 673;
Best Local Similarity 33.3%; Pred. No. 9,9e-55;
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

QY 66 KKKVKRLS----FQRYFNASRLRGITPOAPRLHLLDEDTLGOARHMLSKVGMDFDIFL 121
DB 218 KKKKKRPMQISGVKKLMHSSSLTNSIPRGVKTQEDVLAKE--LEDVNMKGHLAVR 274
QY 122 FDRLTNGSLVTLTLC-LFNTHGLIHFKLDVTLHRLVLMVOEDYHSQNPYNNAAVHAD 180
DB 275 IAEI-SGNRPFLVIMHTIFQERDLTFKIPVDTLITLTLEDYHADVAANNHHAAD 333
QY 181 VTQAMHCYKEPKLASFLPLDMLGLAAAHADVDPGVNOPLFKTNHNLNLYQNM 240
DB 334 VQSTHVLSTPLAEVFDLELAIFASAIHDVDPGVSNQFLINTSELAAMYNDSS 393
QY 241 VLENHNRSTIGMLRESR--LNAHLPKEMTQDIEQOLGSLIATDINRONEFLTRKAL 298
DB 394 VLENHNLAVGFKLQENCDIFQNLTKKORSLRKAVIDIVLATDMSKHNMLADLKTW 453
QY 299 HNMD-----LRLEDADRHFMLOIALKCADICNPCRIMESKOMSERVCEERYGELE 352
DB 454 ETKKVTSSGVLLDNYSRQYVLQNNVHCADLSNPKPLQYKQMDRIIMEEFFRGDRE 513
QY 353 QKFELEISPLCNOOKDSIPSIQIGFMSYIPEPLRFREMAHFTGNSLSENNLGHANHAQ 412
DB 514 RERGMEISPMCKHNASVERKSGVGFIDYIVHPLMETWADLVHPD--AQDILDTLEDNREW 571
QY 413 WKSLPQRHRSRSGSGGPDHAGGTSE-----EQEGDS 449
DB 572 YOSTIPQ-----SPSPAPDDPEEGOGOTEKFOFELTLEEDGS 610

RESULT 9
US-08-206-188B-63
Sequence 63, Application US/08206188B
Patent No. 6100025
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/206,188B
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36107
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-206-188B-63

Query Match 25.1%; Score 604.5; DB 3; Length 673;
Best Local Similarity 33.3%; Pred. No. 9, 9e-55;
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

QY 66 KKKVKRLS----FQRYFNASRLRLGIIIPQAPRLHLLDEDEYLQARHMLSKVGMDFDIFL 121
DB 218 KKKRRPMSQISGVKLMHSSLSLNSIPRGVKTQEDVLAKE--LEDVKNMGLHVR 274
QY 122 FDRLTNGNSLVTLCH-LFNTNGLIHFKIDMTLHREFLVMQVEDYHSQNPYHNAVHAAD 180
DB 275 IAEI-SGNRPVLYIMHTIFQERDLTKFKIPVDTLTLYMTLEDYHNAVAHNNHNAAD 333
QY 181 VTQAHCYLKEPKIASFLPLDMLGLAAADVDHPGVNOFELIKTNHNLNLYQNS 240
DB 334 VVOSTHVLSTPALEAVFTLEILAAIFASAIHDVHPGVSNQFLINTSELAFLMNDSS 393
QY 241 VLENHNRSTIGMLRES--LNAHLPKEMTODIEQGLSLIATDINRONEFLTRKALH 298
DB 394 VLENHNLAVGFKLQENCDIFQNLTKKQROSLRKMYIDIVLATDMSKHMNLADLKTMY 453
QY 299 HNKD-----LRLEDAODRHFMQLALCKADICNPCRIMESKOWSERVCEFFYRQGELE 352
DB 454 ETKKVTSSGVLLDNYSDRIQVLMNVCADLSNPTKPIQLYRQMTDRIMEEFFRQGRE 513
QY 353 OKFLEISPLCNOKDSIPSIQIGFMSYIEPLFRMAHFTGNSLSENNGLAHNKAQ 412
DB 514 RERGMEISPMCDKHNASVEKSYGVFTIDYIVHPLMETWADLVHPD--AODILDTLEDNRW 571
QY 413 WKSLPRQHSRSGSGSPDHMAQGTSE-----EQEGDS 449
DB 572 YQSTIPQ-----SPSPAPDDPEBGQGTQKRFQFELTLEEDGS 610

RESULT 10
US-08-577-492-35
Sequence 35; Application US/08577492
Patent No. 5851784
GENERAL INFORMATION:
APPLICANT: Owens, Raymond John
APPLICANT: Perry, Martin John
TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5851784aris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/577,492
FILING DATE: 22-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426227.6
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9512996.1
FILING DATE: 26-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cherry, David A.
REGISTRATION NUMBER: 35,099
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: unknown
US-08-577-492-35

Query Match 24.9%; Score 599.5; DB 2; Length 673;
Best Local Similarity 33.6%; Pred. No. 3, 3e-54;
Matches 136; Conservative 84; Mismatches 152; Indels 33; Gaps 10;

QY 66 KKKVKRLS----FQRYFNASRLRLGIIIPQAPRLHLLDEDEYLQARHMLSKVGMDFDIFL 121
DB 218 KKKRRPMSQISGVKLMHSSLSLNSIPRGVKTQEDVLAKE--LEDVKNMGLHVR 274
QY 122 FDRLTNGNSLVTLCH-LFNTNGLIHFKIDMTLHREFLVMQVEDYHSQNPYHNAVHAAD 180
DB 275 IAEI-SGNRPVLYIMHTIFQERDLTKFKIPVDTLTLYMTLEDYHNAVAHNNHNAAD 333
QY 181 VTQAHCYLKEPKIASFLPLDMLGLAAADVDHPGVNOFELIKTNHNLNLYQNS 240
DB 334 VVOSTHVLSTPALEAVFTLEILAAIFASAIHDVHPGVSNQFLINTSELAFLMNDSS 393
QY 241 VLENHNRSTIGMLRES--LNAHLPKEMTODIEQGLSLIATDINRONEFLTRKALH 298
DB 394 VLENHNLAVGFKLQENCDIFQNLTKKQROSLRKMYIDIVLATDMSKHMNLADLKTMY 453
QY 299 HNKD-----LRLEDAODRHFMQLALCKADICNPCRIMESKOWSERVCEFFYRQGELE 352
DB 454 ETKKVTSSGVLLDNYSDRIQVLMNVCADLSNPTKPIQLYRQMTDRIMEEFFRQGRE 513
QY 353 OKFLEISPLCNOKDSIPSIQIGFMSYIEPLFRMAHFTGNSLSENNGLAHNKAQ 412
DB 514 RERGMEISPMCDKHNASVEKSYGVFTIDYIVHPLMETWADLVHPD--AODILDTLEDNRW 571
QY 413 WKSLPRQHSRSGSGSPDHMAQGTSE-----EQEGDS 449
DB 572 YQSTIPQ-----SPSPAPDDPEBGQGTQKRFQFELTLEEDGS 610

RESULT 11
US-09-079-630-35
Sequence 35; Application US/09079630
Patent No. 6291199
GENERAL INFORMATION:
APPLICANT: Owens, Raymond John
APPLICANT: Perry, Martin John
TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
NUMBER OF SEQUENCES: 40

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6291199ris
;; STREET: One Liberty Place, 46th floor
;; City: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 6.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/079,630
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/577,492
;; FILING DATE: 22-DEC-1995
;; APPLICATION NUMBER: GB 9426227.6
;; FILING DATE: 23-DEC-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9512996.1
;; FILING DATE: 26-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cherry, David A.
;; REGISTRATION NUMBER: 35,099
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 35:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 673 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;;
US-09-079-630-35

Query Match 24.9%; Score 599.5; DB 4; Length 673;
Best local Similarity 33.6%; Pred. No. 3.3e-54;
Matches 136; Conservative 84; Mismatches 152; Indels 33; Gaps 10;

QY 66 KKKVKRLS---FQRYFNASRLRGIIIPQAPLHLDEEDYLGQARHMLSKVGMWDDIFL 121
DB 218 KKKKQPMQISGVKKLMHSSSLNFSIRFGVKTGEQEDVLAKE---LEQVNMKGHLVFR 274

QY 122 FDLTLGNSLVTLCH-LENTHGLIHFKLDVTLHRLVWQEDYHSQNPYHNAVAHAD 180
DB 275 IABL-SGNRPGLVIMHTIFQERDLTKTKFIPVDTLITVMTLDDHYHADVAHNNIHAAD 333

QY 181 VTQAMCYLKEPKLASFLTPDLIMGLLAAAHADVHDHGVSNQPLTKTNHHLNLYQMS 240
DB 334 VQSTHVLSTPALDAVFTDLEILAAIFASAHIDVDHGVSNQPLINTNSLALMTNDSS 393

QY 241 VLENHNRSTIGMLRESR--LLAHLPEKMTODIEQUGSLIATDINRQNEFLTRLKAHL 298
DB 394 VLENHHLAVGFKLQGEHCDFQNLTKKQKQSLRKMYIDIVLATDKSKHNNLADLKTWY 453

QY 299 HAKD-----LLEDAODRHFMQLALCADICNPCRIMWSKQWSRVCEEFYRQGELE 352
DB 454 ETKKVTSSGVLLDNYSDRIQVLNNVHCADLSNPKRPLQLYROMWDRIMEEFFFFQGDRE 513

QY 353 QKFELEISPLCNOQKDSIPSIQIGFMSYIEPLFERNAHFTGNSLTSENNLGLAHNAKAQ 412
DB 514 RKGMEISPMCDKHNASVSKQVGFIDYIVHPLMETWADLVQPD--AQDILDTLEDNRWY 571

QY 413 WKSILPRQHRSGSSGSPDHAG-OGTRESF-----EQEGDS 449
DB 572 YQSTIPQ-----SPSPAPDDPEGRGQGTGKFOFELTLEEDGS 610

RESULT 12
US-07-688-352C-4

;; Sequence 4, Application US/07688352C
;; Patent No. 5527896
;;
;; GENERAL INFORMATION:
;; APPLICANT: Wigler, Michael H.
;; APPLICANT: Colicelli, John J.
;; TITLE OF INVENTION: Cloning by Complementation and Related
;; TITLE OF INVENTION: Processes
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;; STREET: Two First National Plaza, 20 South Clark
;; STREET: Street
;; City: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60603
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/688,352C
;; FILING DATE: 19910419
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/511,715
;; FILING DATE: 20-APR-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Borun, Michael F.
;; REGISTRATION NUMBER: 25447
;; REFERENCE/DOCKET NUMBER: 27805/30197
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 346-5750
;; TELEFAX: (312) 984-9740
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 562 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-07-688-352C-4

Query Match 24.1%; Score 580.5; DB 1; Length 562;
Best local Similarity 31.9%; Pred. No. 2.5e-52;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

QY 66 KKKVKRLS---FQRYFNASRLRGIIIPQAPLHLDEEDYLGQARHMLSKVGMWDDIFL 121
DB 124 KKKQQLMTQISGVKKLMHSSSLNFTSISRFVNTENEDHLAKLEDLKN---WGLITFN 180

QY 122 FDLTLGNSLVTLCHLFTNHGILHFKLDVTLHRLVWQEDYHSQNPYHNAVAHAD 181
DB 181 VAGYSNRPGLTCMAVLFQGRDLTKTKFKISDFVYIMMTLEHHSYSDVAHNSLAHADY 240

QY 182 TQAMCYLKEPKLASFLTPDLIMGLLAAAHADVHDHGVSNQPLTKTNHHLNLYQMSV 241
DB 241 AOSTHVLSTPALDAVFTDLEILAAIFAAAHIDVDHGVSNQPLINTNSLALMYNDESV 300

QY 242 LLENHNRSTIGMLRESR--LLAHLPEKMTODIEQUGSLIATDINRQNEFLTRLKAHL 299
DB 301 LLENHHLAVGFKLQGEHCDFQNLTKKQKQSLRKMYIDIVLATDKSKHNSLADLKTWY 360

QY 300 NKD-----LLEDAODRHFMQLALCADICNPCRIMWSKQWSRVCEEFYRQGELE 353
DB 361 TKKVTSSGVLLDNYSDRIQVLNNVHCADLSNPKRPLQLYROMWDRIMEEFFFFQGDKER 420

QY 354 KFELEISPLCNOQKDSIPSIQIGFMSYIEPLFERNAHFTGNSLTSENNLGLAHNAKAQ 413
DB 421 ERGMEISPMCDKHNASVSKQVGFIDYIVHPLMETWADLVQPD--AQDILDTLEDNRWY 478

OY 414 KSLPR-----QHRSGSSGSGPBDH-----AGGTSESEOGDSP 450
Db 479 QSMFQSPSPPLDRSRDCGLMKEKFOFELTLEEDSEGEKGECP 525

RESULT 13

US-08-942-521B-8
; Sequence 8, Application US/08942521B
; Patent No. 5932477
; GENERAL INFORMATION:
; APPLICANT: Livi, George P.
; APPLICANT: McLaughlin, Megan M.
; APPLICANT: Torphy, Theodore J.
; TITLE OF INVENTION: Human Brain Phosphodiesterase
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Patents/P.O.Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/942,521B
; FILING DATE: October 2, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,386
; FILING DATE: 22 May 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,334
; FILING DATE: 10 March 1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth J. Hecht
; REGISTRATION NUMBER: 41,824
; REFERENCE/DOCKET NUMBER: P50145C1FMC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5009
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-942-521B-8

Query Match 24.1%; Score 580.5; DB 2; Length 562;
Best Local Similarity 31.9%; Pred. No. 2,5e-52;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

OY 66 KKKYKRLS----FORFHASRLRGITIPQAPHLHLEDEYLGQARRHMSKVGMMDFDIL 121
Db 124 KKKQOQLMTQISGVKALHSSLNNTSISRFQVTEHEDHLAELEDLNK--WGINTFN 180
OY 122 FDRLTNGNSLVTLCPLFNHGLIHNRKLDVTLHRELNVWQEDYNSQNPYNAVAADY 181
Db 181 VAGSYHNRPLTCIMYALFQERDLTKTFKISSDFVYVMTELDHYSDDVAYHNSLHAADY 240
OY 182 TOAMHCYLKBEKSLASFLTPDLIMGLIAAANDVDHPGVNQPLIKTNHHLANLYONMSV 241
Db 241 AOSTHVLSTPDLDAVFTDELLAIFAAAIHVDPGVSNQPLINTNSELLAMYNDESV 300
OY 242 LENHWRSTIGMLRESR--LLAHLPKEMTODIEQOLGSLILANDINRQNEFLRLKANH 299

Db 301 LENHHLAVGERLLLOEEHCDFQNLTKKOROTLKRKVIDWLVATDMKHNHSLADLKTWE 360
OY 300 NKD-----LLEFQADNRHFMLOIALKCADICNCRITWMSQWSEVCEFFYRQGELEQ 353
Db 361 TKKYTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLLEYRQWDRIMEFFFOQDKER 420
OY 354 KFELEIPLCNOCKDSIPSIQIGMSYVPLFREMAHFTGNSTSENNLGHLANRQW 413
Db 421 ERGMEISPMCDKHTASVEKSOVGFDIYVHPMETWADLVQPD--AQDILDFLEDRNMY 478
OY 414 KSLPR-----QHRSGSSGSGPBDH-----AGGTSESEOGDSP 450
Db 479 QSMFQSPSPPLDRSRDCGLMKEKFOFELTLEEDSEGEKGECP 525

RESULT 14

US-08-474-379C-4
; Sequence 4, Application US/08474379C
; Patent No. 5977305
; GENERAL INFORMATION:
; APPLICANT: Wiegler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,379C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/206,188
; FILING DATE: 01-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,352
; FILING DATE: 19-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 27866/32771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-379C-4

Query Match 24.1%; Score 580.5; DB 2; Length 562;
Best Local Similarity 31.9%; Pred. No. 2,5e-52;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

OY 66 KKKYKRLS----FORFHASRLRGITIPQAPHLHLEDEYLGQARRHMSKVGMMDFDIL 121
Db 124 KKKQOQLMTQISGVKALHSSLNNTSISRFQVTEHEDHLAELEDLNK--WGINTFN 180
OY 122 FDRLTNGNSLVTLCPLFNHGLIHNRKLDVTLHRELNVWQEDYNSQNPYNAVAADY 181
Db 181 VAGSYHNRPLTCIMYALFQERDLTKTFKISSDFVYVMTELDHYSDDVAYHNSLHAADY 240
OY 182 TOAMHCYLKBEKSLASFLTPDLIMGLIAAANDVDHPGVNQPLIKTNHHLANLYONMSV 241
Db 241 AOSTHVLSTPDLDAVFTDELLAIFAAAIHVDPGVSNQPLINTNSELLAMYNDESV 300
OY 242 LENHWRSTIGMLRESR--LLAHLPKEMTODIEQOLGSLILANDINRQNEFLRLKANH 299

Db 124 KKKKQOLMTOISGVKKLMHSSSLNNTSISRFVNTENEDHLAKLEDLNK---WGLNIFN 180
 QY 122 FDLRTGNSLVTLCLHFTNGLIHFFKLDWTLHFRFLVWODVYHSQPNYNAVAADY 181
 Db 181 VAGYSNRPILTCIMTAIFQERDLTKTKISDFTVTYMMTLEDHYSDAVAHNSLAADY 240
 QY 182 TQAMHCYLKEPKLASEFLPLDLMGLLAAAHVDHDPGVNOPELTKTNHNLANYOMSV 241
 Db 241 AOSTHVLLSTPALDAVFTDEILAAIFAAAHVDHDPVSNQFLINTNSLALMYNDESV 300
 QY 242 LENHHNRSTIGMLRESR--LHAHPKEMTODIEQUGSLILATDIRONEFLTRKAHLH 299
 Db 301 LENHHLAVGEFKLQEHCDIFQNLTKRKQOTLKKWIDWVLAIDMSKHSLLADLKTWVE 360
 QY 300 NKD-----LRLDAQDRHFMLOIALKCADICNCRIFWMSKOWSRVCEEFYRQGELO 353
 Db 361 TKKVTSSGVLLDNTDRIOVLNNVHCADLSNPTLSLEYROWTDRIEERFQGDKER 420
 QY 354 KELEISPLCNOQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSLSENNLGHLANHKAOW 413
 Db 421 ERGMEISPMCDKHTASVEKSQYGFIDYIYHPLMETWADLVQPD--AQDILDTLEDNRNY 478
 QY 414 KSLLP-----QHSRSGSSGSPDDH---AGCTESEBDEGDS 450
 Db 479 OSMIPQSPPLDERSRDCQGLMEKFOFELTLEEDSEGEPEKGESE 525

RESULT 15
 US-09-146-249A-4
 ; Sequence 4, Application us/09146249A
 ; Patent No. 6069240
 ; GENERAL INFORMATION:
 ; APPLICANT: Wigler, Michael H.
 ; APPLICANT: Colicelli, John J.
 ; TITLE OF INVENTION: Cloning by Complementation and Related
 ; TITLE OF INVENTION: Processes
 ; NUMBER OF SEQUENCES: 85
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/146,249A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/511,715
 ; FILING DATE: 20-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ. ID NO.: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 562 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-146-249A-4

Query Match

24.1%; Score 580.5; DB 3; Length 562;

Best Local Similarity 31.9%; Pred. No. 2,5e-52;
 Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

QY 66 KKKKRLLS-----FQFYFASRLRGIIPQAPLHLIDEDYLGQARMLSKVGMPDIFL 121
 Db 124 KKKKQOLMTOISGVKKLMHSSSLNNTSISRFVNTENEDHLAKLEDLNK---WGLNIFN 180
 QY 122 FDLRTGNSLVTLCLHFTNGLIHFFKLDWTLHFRFLVWODVYHSQPNYNAVAADY 181
 Db 181 VAGYSNRPILTCIMTAIFQERDLTKTKISDFTVTYMMTLEDHYSDAVAHNSLAADY 240
 QY 182 TQAMHCYLKEPKLASEFLPLDLMGLLAAAHVDHDPGVNOPELTKTNHNLANYOMSV 241
 Db 241 AOSTHVLLSTPALDAVFTDEILAAIFAAAHVDHDPVSNQFLINTNSLALMYNDESV 300
 QY 242 LENHHNRSTIGMLRESR--LHAHPKEMTODIEQUGSLILATDIRONEFLTRKAHLH 299
 Db 301 LENHHLAVGEFKLQEHCDIFQNLTKRKQOTLKKWIDWVLAIDMSKHSLLADLKTWVE 360
 QY 300 NKD-----LRLDAQDRHFMLOIALKCADICNCRIFWMSKOWSRVCEEFYRQGELO 353
 Db 361 TKKVTSSGVLLDNTDRIOVLNNVHCADLSNPTLSLEYROWTDRIEERFQGDKER 420
 QY 354 KELEISPLCNOQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSLSENNLGHLANHKAOW 413
 Db 421 ERGMEISPMCDKHTASVEKSQYGFIDYIYHPLMETWADLVQPD--AQDILDTLEDNRNY 478
 QY 414 KSLLP-----QHSRSGSSGSPDDH---AGCTESEBDEGDS 450
 Db 479 OSMIPQSPPLDERSRDCQGLMEKFOFELTLEEDSEGEPEKGESE 525

Search completed: September 13, 2002, 12:05:51
 Job time: 252 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 11:59:44 : Search time 31.9 Seconds
(without alignments)
1566.872 Million cell updates/sec

Title: US-09-471-459A-5

Perfect score: 2408

Sequence: 1 MSCLMVENCSEILFENPDQN.....PDHDAAGGTSEEGEDGSP 450

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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15: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1994.DAT:*
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18: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2408	100.0	450	21	AA93569	Amino acid sequenc
2	2408	100.0	450	22	AA678915	Human type 7B phos
3	2408	100.0	450	22	AA008675	Human phosphodiester
4	2234	92.8	502	22	AA836503	Human long phospho
5	2219.5	92.2	451	21	AA93575	Amino acid sequenc
6	2192	90.0	446	21	AA93567	Amino acid sequenc
7	2166	90.0	446	21	AA93574	Amino acid sequenc
8	2165.5	89.9	445	21	AA93573	Amino acid sequenc
9	2121	88.1	437	21	AA93572	Amino acid sequenc
10	1990.5	82.7	413	21	AA93571	Amino acid sequenc
11	1865	77.5	391	22	AA008676	Human phosphodiester

12	1430	59.4	268	21	AA93593	Amino acid sequenc
13	1430	59.4	288	21	AA93568	Amino acid sequenc
14	1419.5	58.9	498	17	AA000094	CAMP phosphodiester
15	1419.5	58.9	498	20	AA49808	Human glioblastoma
16	1419.5	58.9	498	21	AA520619	PTM22 human gliobl
17	1286	53.4	432	22	AA016967	Human novel secret
18	1280	53.2	320	22	AA836504	Human short phosph
19	771	32.0	211	22	AA023004	Novel human enzyme
20	771	32.0	211	22	AA018681	Renal and cardiora
21	771	32.0	211	22	AA017039	Human novel secret
22	604.5	25.1	507	21	AA93995	Human novel secret
23	604.5	25.1	518	22	AA661185	Human PDE4D6 prote
24	604.5	25.1	673	20	AA498827	Human PDE4D6-like p
25	604.5	25.1	673	21	AA820638	pppG43 human dunce
26	604.5	25.1	673	21	AA93997	Amino acid sequenc
27	604.5	25.1	673	22	AA51411	Human phosphodiester
28	604.5	25.1	704	22	AB606964	Novel human diagno
29	604.5	25.1	745	21	AA93996	Amino acid sequenc
30	604.5	25.1	929	22	AA65780	Amino acid sequenc
31	604.5	25.1	930	21	AA84876	Amino acid sequenc
32	604.5	25.1	1002	21	AA84878	Amino acid sequenc
33	604.5	25.1	1066	21	AA84877	Amino acid sequenc
34	603.5	25.1	517	22	AA661186	Rat PDE4D6 protein
35	599.5	24.9	674	17	AA89743	Human phosphodiester
36	598.5	24.9	1029	22	AA65779	Amino acid sequenc
37	580.5	24.1	562	12	AA014836	"Dunce"-like phosph
38	580.5	24.1	562	17	AA000090	Rat dunce-like pro
39	580.5	24.1	562	20	AA49803	Rat dunce-like pro
40	580.5	24.1	562	21	AA820614	Plasamid PRATPD 2.
41	580.5	24.1	564	22	AAE04745	Rat CAMP-specific
42	580.5	24.1	659	22	AAE04741	Rat CAMP-specific
43	580.5	24.1	721	22	AAE04746	Rat CAMP-specific
44	580.5	24.1	736	22	AAE04743	Rat CAMP-specific
45	567.5	23.6	564	15	AA860605	Brain low Km, CAMP

ALIGNMENTS

RESULT 1	
AA93569	standard; Protein; 450 AA.
XX	
AC	AA93569;
XX	
DT	25-SEP-2000 (first entry)
XX	
DE	Amino acid sequence of a human phosphodiesterase enzyme.
XX	
KM	Phosphodiesterase; PDE-XIV; human; enzyme.
XX	
OS	Homo sapiens.
XX	
PN	EP1018559-A1.
XX	
PD	12-JUL-2000.
XX	
PF	09-NOV-1999; 99EP-0308902.
XX	
PR	23-DEC-1998; 98GB-0028603.
PR	17-SEP-1999; 99GB-0022123.
XX	
PA	(PFIZ) PFIZER LTD.
PA	(PFIZ) PFIZER INC.
PI	Fidock M:
XX	
DR	WPI; 2000-433274/38.
DR	N-PSDB; AAA46651.
XX	
PT	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT	useful for preventing diagnosing and treating diseases associated with
PT	inappropriate PDE-XIV expression and/or activity -

XX Disclosure; Page 45-47; 104pp; English.

PS
XX
CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC be administered to treat diseases by rectifying mutations or deletions
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV agonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

XX Sequence 450 AA:

Query Match 100.0%; Score 2408; DB 21; Length 450;
Best Local Similarity 100.0%; Pred. No. 2,3e-227;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCIAWRCGELLFENPDONAKVCMLDILRGOTGVRAERKSGYFIDFLLNSTTYS 60
DB 1 msciawrcgellfepndpnakvcmlgdilrgotgvraerksygidfllnsttys 60
OY 61 GEIGTKKKVKRLSFOYFHASRLRGLIPQAPRLHLDDEYLGQARHMLSKVGMDFDIF 120
DB 61 geigtkkkvkrllsforyfhasrlrlgllpqaprlhlldedylgqarhmlskvgmddfif 120
OY 121 LFDRLTNGNSLVTLCHLFTNTHGLIHHFKLDVTLHRLFLVWQEDYHSQNPYHNAVHAD 180
DB 121 lfdrltngnslvtlchlftnthglihhfkldvtlhrlflvmwgedyhsqnpynhavhad 180
OY 181 VTQAMHCYIKERPKLASFLTPDLMGLAAAHADVDPVNOPLTKTNHNLANYQNS 240
DB 181 vtqamhcylkerpklasfltpdlmglaaaahadvdpvnopltktnhnlanyqns 240
OY 241 VLENHNRSTIGMLRESRLLAHLRKEMTODIEQGLSLIATDINRONEFLTRKALHNLN 300
DB 241 vlenhnrstigmlesrllahlrkemtodieqglslilatdinronefltrkahlhnl 300
OY 301 KDLRLDAODRHFMLOIALKCADICNPCRIMESKOWSERVCEEFYRQGLEOKFELEIS 360
DB 301 kdrlledaodrhmloialkcadicnprcrlwmskwservceefyrqgleokfeleis 360
OY 361 PLCNOOKDIPSIQIGFMSYIYVPLFRMAHFTGNSITSENMLGHLAHNAQWKSLLPRQ 420
DB 361 plcnookdipsiqigfmsyiyvplfrmahftgnsitsemnlghlahnkaqwkslprq 420
OY 421 HRSRSGSGSPDHDAAGTSEFEOGDSR 450
DB 421 hrsrsgsgspdhdaagtseefegdsr 450

RESULT 2

AA078915
ID AAG78915 standard; protein; 450 AA.

XX AAG78915:

XX 19-DEC-2001 (first entry)

XX Human type 7B phosphodiesterase, PDE7B.

KW Human; type 7B phosphodiesterase; PDE7B; enzyme.

XX OS . Homo sapiens.

XX JP2001238680-A.

XX 04-SEP-2001.

XX 03-MAR-2000; 2000JP-0058159.

XX 03-MAR-2000; 2000JP-0058159.

XX (TANA) TANABE SEIYAKU CO.

XX WPI: 2001-610057/70.

XX N-PSDB: AA170009.

XX Claim 2; Page 12-14; 18pp; Japanese.

CC The present sequence is the protein sequence for human type 7B
CC phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the
CC development of inhibitors of high selectivity and drugs of low side
CC effects.

XX Sequence 450 AA:

Query Match 100.0%; Score 2408; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 2,3e-227;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCIAWRCGELLFENPDONAKVCMLDILRGOTGVRAERKSGYFIDFLLNSTTYS 60
DB 1 msciawrcgellfepndpnakvcmlgdilrgotgvraerksygidfllnsttys 60
OY 61 GEIGTKKKVKRLSFOYFHASRLRGLIPQAPRLHLDDEYLGQARHMLSKVGMDFDIF 120
DB 61 geigtkkkvkrllsforyfhasrlrlgllpqaprlhlldedylgqarhmlskvgmddfif 120
OY 121 LFDRLTNGNSLVTLCHLFTNTHGLIHHFKLDVTLHRLFLVWQEDYHSQNPYHNAVHAD 180
DB 121 lfdrltngnslvtlchlftnthglihhfkldvtlhrlflvmwgedyhsqnpynhavhad 180
OY 181 VTQAMHCYIKERPKLASFLTPDLMGLAAAHADVDPVNOPLTKTNHNLANYQNS 240
DB 181 vtqamhcylkerpklasfltpdlmglaaaahadvdpvnopltktnhnlanyqns 240
OY 241 VLENHNRSTIGMLRESRLLAHLRKEMTODIEQGLSLIATDINRONEFLTRKALHNLN 300
DB 241 vlenhnrstigmlesrllahlrkemtodieqglslilatdinronefltrkahlhnl 300
OY 301 KDLRLDAODRHFMLOIALKCADICNPCRIMESKOWSERVCEEFYRQGLEOKFELEIS 360
DB 301 kdrlledaodrhmloialkcadicnprcrlwmskwservceefyrqgleokfeleis 360
OY 361 PLCNOOKDIPSIQIGFMSYIYVPLFRMAHFTGNSITSENMLGHLAHNAQWKSLLPRQ 420
DB 361 plcnookdipsiqigfmsyiyvplfrmahftgnsitsemnlghlahnkaqwkslprq 420
OY 421 HRSRSGSGSPDHDAAGTSEFEOGDSR 450
DB 421 hrsrsgsgspdhdaagtseefegdsr 450

RESULT 3

AA008675
ID AA008675 standard; protein; 450 AA.

XX AA008675:

DT 18-DEC-2001 (first entry)
 XX
 DE Human phosphodiesterase type 7B #1.
 XX
 KW Human; phosphodiesterase type 7B; cardiovascular disease;
 KW asthma; allergy; inflammatory disease; immune-related disorder;
 KW cardiovascular; antiallergic; antiallergic; immunosuppressive;
 KW antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 PN WO200162940-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-EP01858.
 XX
 PR 21-FEB-2000; 2000EP-0103655.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Kluxen F, Hentsch B;
 XX
 DR WPI; 2001-570636/64.
 DR N-PSDB; AAS13248.
 XX
 PT Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,
 PT diagnosing and treating, e.g. asthma, inflammation and allergies -
 XX
 PS Claim 1; Page 36-37; 40pp; English.
 XX
 CC The invention relates to a novel human phosphodiesterase type 7B
 CC polypeptide and the nucleic acid that encodes it. The protein and nucleic
 CC acid may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate phosphodiesterase 7B (P7B) expression. For
 CC example, the protein and nucleic acid may be used to treat
 CC disorders associated with decreased expression by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of P7B by
 CC expressing inactive proteins or to supplement the patients own
 CC production of P7B. The nucleic acids may be used to produce P7B
 CC polypeptides, by inserting the nucleic acids into a host cell and
 CC culturing the cell to express the protein. The nucleic acid and its
 CC complements may also be used as DNA probes in diagnostic assays to detect
 CC and quantitate the presence of similar nucleic acids in samples, and
 CC therefore which patients may be in need of restorative therapy. The P7B
 CC polypeptides may also be used as antigens in the production of
 CC antibodies against P7B and in assays to identify modulators of it's
 CC expression and activity. The anti-P7B antibodies and antagonists may
 CC also be used to down regulate expression and activity. The anti-P7B
 CC antibodies may also be used as diagnostic agents for detecting the
 CC presence of P7B in samples (e.g. by enzyme linked immunosorbent assay
 CC (ELISA)). Disorders that may be prevented, diagnosed and/or treated by
 CC the above methods include, for example cardiovascular disease, asthma,
 CC allergy, inflammation, and immune-related disorders. The present
 CC sequence represents a human phosphodiesterase 7B.
 XX
 SQ Sequence 450 AA:

Query Match 100.0%; Score 2408; DB 22; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.3e-22;
 Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLWVREGCETLEFNDPQNAKVCMLGDIRLNGOTGVAERGSVPFDRLNSTYS 60
 DB 1 MSLWVREGCETLEFNDPQNAKVCMLGDIRLNGOTGVAERGSVPFDRLNSTYS 60
 QY 61 GEIGTKKKVKRLSPQRYFHASRLNGIIPQAPLHLDELDYLGQAHHMLSKVGMDFDF 120
 DB 61 GEIGTKKKVKRLSPQRYFHASRLNGIIPQAPLHLDELDYLGQAHHMLSKVGMDFDF 120
 QY 121 LFDRLTNGSLVTLCHLEFNTGCLHHEFKLDWVTLHREPLVMOEDYHSQNPYHNAVAAD 180
 DB 121 LFDRLTNGSLVTLCHLEFNTGCLHHEFKLDWVTLHREPLVMOEDYHSQNPYHNAVAAD 180

DB 121 lfdrltngslvllchlefnthbgljnhfkldwvclhrlvmvgedyhsqnpynavaad 180
 QY 181 VTOAMHCYLKEPKLASFLTRPDIMGCLLAAADVDVHREGVNPFLLKTHHHLANLYQNN 240
 DB 181 VTOAMHCYLKEPKLASFLTRPDIMGCLLAAADVDVHREGVNPFLLKTHHHLANLYQNN 240
 QY 241 VLENHHWRSTIGMLRESRLAHLPKEMTODIEQOLSLIATDINQNFTRFLKHAHLN 300
 DB 241 VLENHHWRSTIGMLRESRLAHLPKEMTODIEQOLSLIATDINQNFTRFLKHAHLN 300
 QY 301 KDRLLEDADRHFMLOIALKADICNPICRIWKSQMSRVCBEFYRGCELEQEFLEIS 360
 DB 301 KDRLLEDADRHFMLOIALKADICNPICRIWKSQMSRVCBEFYRGCELEQEFLEIS 360
 QY 361 PLCNOOKDSIPSTQGFMSYIVPELRFRENAHFTGNTLSNNMIGHLAHNAKMKSLPRQ 420
 DB 361 PLCNOOKDSIPSTQGFMSYIVPELRFRENAHFTGNTLSNNMIGHLAHNAKMKSLPRQ 420
 QY 421 HRSRGSSSGSPDHDAOGCTESEDEQDSDP 450
 DB 421 HRSRGSSSGSPDHDAOGCTESEDEQDSDP 450

RESULT 4
 AAB36503
 ID AAB36503 standard; Protein; 502 AA.
 XX
 AC AAB36503;
 XX
 DT 06-MAR-2001 (first entry)
 XX
 DE Human long phosphodiesterase protein SEQ ID NO.1.
 XX
 KW Human; long phosphodiesterase; short phosphodiesterase; diagnosis;
 KW cyclic nucleotide phosphodiesterase; nootropic; cardiant; hypotensive;
 KW nephrotropic; antidepressant; antiinflammatory; immunosuppressive;
 KW antiinflammatory; antiallergic; vasotropic; gene therapy; dementia;
 KW amnesia; congestive heart failure; thrombosis; pulmonary hypertension;
 KW glomerulonephritis; bipolar depression; bronchial asthma; salt retention;
 KW atopic disease; autoimmune encephalomyelitis; organ transplantation;
 KW nephrotic syndrome; erectile dysfunction.
 XX
 OS Homo sapiens.
 XX
 PN US6146876-A.
 XX
 PD 14-NOV-2000.
 XX
 PF 11-JUN-1999; 99US-0330970.
 XX
 PR 26-MAR-1999; 99US-0277423.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Kapeller-Libermann R, White D, Robison KE;
 XX
 DR WPI; 2001-023577/03.
 DR N-PSDB; AAC87948.
 XX
 PT Polynucleotide encoding novel cyclic nucleotide phosphodiesterase
 PT useful for treating disorders related with to protein e.g. dementia,
 PT hypertension, glomerulonephritis, and organ transplantation -
 XX
 PS Claim 3; Fig 1; 42pp; English.
 XX
 CC The present sequence represents the human long phosphodiesterase which
 CC is a cyclic nucleotide phosphodiesterase (1). (1) can have nootropic,
 CC cardiant, hypotensive, nephrotropic, antidepressant, antiinflammatory,
 CC immunosuppressive, antiinflammatory, antiallergic and vasotropic
 CC activities, and can be used in gene therapy. (1) can be used for
 CC treating various disorders associated or mediated by (1), such as
 CC dementia, amnesia, congestive heart failure, thrombosis, pulmonary
 CC hypertension, glomerulonephritis, bipolar depression, bronchial asthma,

CC atopic diseases, autoimmune encephalomyelitis, organ transplantation,
 CC salt retention in nephrotic syndrome and erectile dysfunction.

XX Sequence 502 AA:

Query Match 92.8%; Score 2234; DB 22; Length 502;
 Best Local Similarity 99.1%; Pred. No. 3.1e-210;
 Matches 419; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 28 GDIRLRGQTVRAERRGSTPYDFERLNLSTTSGEIGTKKKKRLLSFORFHASRLRG 87
 DB 80 gdlrlrqlgvrnaerrgsyplfdfrllnstysgeigkkrllsfqrfhasrllrg 139
 OY 88 IIPQAPLHLDEDYLGQARHMLSKGWMDFIPLFDRRTNGNSLVTLCHLPHNGLIHH 147
 DB 140 iipqaplhlldedylgqarhmlskgwmdfdlfdrtrngnsivtlchlfnhglilh 139
 OY 148 EKIDAWTLHRELVMQEDYHSQNPYHNAVDYQAMHCYKRPKIASPLTPIMLGL 207
 DB 200 fklmwtlhrflvmqedyhsqnpynavdaavqamncykrepkiasfltpdlmgl 259
 OY 208 LAAAHADVDPVGNOPFLIKTNHLLANLYQNMSTVLENNHNRSTIGMLRESRLAHLPEKM 267
 DB 260 laaahadvdpvgnopfliktnhllanlyqnmstvlenhnrstlglmlrestlahlpkem 319
 OY 268 TQDIEQGLSLTLATDINRQNEFLTRKALHLNKLRLDQAQDRHMLQIALKCADICNP 327
 DB 320 tqdieqglsltlatdinrqnelftrkahlhnlkrlledaqdrlmglawcadicnp 379
 OY 328 CRIEWSKOMSERVCEEFYRQGELEKQFLEISPLCNOOKDSIPSIOIGMSYIVPELFR 387
 DB 380 criewskomservceefyrqgeleqkfelisplcnokdsipsiqigfmsyivpeflfr 439
 OY 388 EWAHFGNSTLSENNLGHIAHNKAQWKSILPROHRSRSGSGGDHAGCGTSEEOEG 447
 DB 440 ewahfgnstlsennlghlahnkaqkwlprhnrstrsgsggdhagcgteseeqeg 499
 OY 448 DSP 450
 DB 500 dsp 502

RESULT 5

AA93575
 ID AA93575 standard: Protein: 451 AA.

XX AA93575;

XX 25-SEP-2000 (first entry)

XX Amino acid sequence of a phosphodiesterase enzyme.

XX Phosphodiesterase: PDE-XIV; enzyme.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 12 /label= Val, Ile

XX Misc-difference 16 /label= Ser, Asn

XX Misc-difference 18 /label= Glu, Asp

XX Misc-difference 20 /label= Ser, Val, Asn, Ala

XX Misc-difference 21 /label= Ser, Val, Asn, Ala

XX Misc-difference 30 /label= Val, Ile

XX Misc-difference 39 /label= Pro, Arg

XX Misc-difference 56

FT /label= Asn, Ser
 FT Misc-difference 59
 FT /label= His, Tyr
 FT Misc-difference 114
 FT /label= Thr, Met
 FT Misc-difference 141
 FT /label= Ser, Thr
 FT Misc-difference 168
 FT /label= Gly, His, Ser, Gln
 FT Misc-difference 169
 FT /label= Gly, His, Ser, Gln
 FT Misc-difference 307
 FT /label= Asp, Ala, Asn, Val
 FT Misc-difference 308
 FT /label= Asp, Ala, Asn, Val
 FT Misc-difference 350
 FT /label= Glu, Asp
 FT Misc-difference 379
 FT /label= Ser, Thr
 FT Misc-difference 391
 FT /label= His, Arg
 FT Misc-difference 404
 FT /label= Gly, Ser
 FT Misc-difference 418
 FT /label= Pro, Arg, Ser, Asn
 FT Misc-difference 419
 FT /label= Pro, Arg, Ser, Asn
 FT Misc-difference 423
 FT /label= Ser, Arg
 FT Misc-difference 435
 FT /label= His, Leu
 FT Misc-difference 438..440
 FT /note= "these residues are either Gln-Gly-Pro or Pro-Ala-Pro"
 FT Misc-difference 442..443
 FT /note= "these residues are either Ser-Glu or Thr-Leu"
 FT Misc-difference 446
 FT /note= "optionally absent"
 FT Misc-difference 449..450
 FT /note= "these residues are either Asp-Ser or Ala-Thr"

EP1018559-A1.

12-JUL-2000.

09-NOV-1999; 99EP-0308902.

23-DEC-1998; 98GB-0028603.

17-SEP-1999; 99GB-0022123.

(PF12) PFIZER LTD.

(PF12) PFIZER INC.

Fidock M;

WPI; 2000-433274/38.

Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity

Disclosure; Page 75-78; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.
 CC The enzyme sequence is derived from a formula of the invention. The
 CC phosphodiesterase polynucleotide and polypeptide may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate PDE-XIV expression. For example, the polynucleotide
 CC be administered to treat diseases by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of PDE-XIV. They may
 CC also be used to study the expression and function of PDE-XIV

CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

XX Sequence 451 AA;

Query Match 92.2%; Score 2219.5; DB 21; Length 451;
Best Local Similarity 93.1%; Pred. No. 7.1e-209;
Matches 420; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

QY 1 MSCLMVERGCELLFENPDNAKVCVMIGDTRLGOTGVRAERGSYPFDIFRLNSTYTS 60
DB 1 mscImvercgevlfeexpqxxkvcvcmldgvdrltqgvgvaerqsyypfdifrlnstx 60
QY 61 GEIGTKKKVRLSFQRYFHASRLRGIIPOAPDLHLDEDDYLGOARHMLSKVGMDFDIF 120
DB 61 geigtkkkvrlsfqryfhassrlrgiipqapdlhldegylsqarhmlskvgwdtdif 120
QY 121 LFDRLTNGNSLVTLCHLFTNGLIHFKIDMYTLHREFLWVOEDYHSQNPYNAVAHAD 180
DB 121 lfdrltngnslvtllchlfntghlhfkdmytlhrfelmvoedyhsnpynavaaad 180
QY 181 VFOAMHCYLKEPKLASFLPDLIMLGILAAADVDHDPGVNOFLRTKTNHILANLVONMS 240
DB 181 vfoamhcylkepklaasflpdlimlgilaaadvdhpyvngflfktknhienlyqms 240
QY 241 VLENHHWRSTIGMLRESRLAHLPRKEMTODIEQOLSLIATDINRONEFLTRLKAHLN 300
DB 241 vlenhhwrstigmresrllahlprkemtodieqolsliatdinronefltrlkahlhn 300
QY 301 KDLRLDADNRHMLQIALKADICNPCTRIMWSKQWSEVCEFFRQGLEQKFELEIS 360
DB 301 kdrlrlexddrhmqlalalcadlcnpctrimwskqwservceeffyrqgleqkfeleis 360
QY 361 PLCNQOKDSTPSIOIGFMSYIVPELRFRENAHFNGNSTLSNMGLAHNAKQKSLPRQ 420
DB 361 plcnqokdsipsiqigfmyiveplrfrewaxftgnstlsenmlshlahnakqksslxxq 420
QY 421 HRSRGSSGSGPDHDHAGOGTESEEO-EGDSP 450
DB 421 hrsgsgsgpdhdhagogteeseo-egdsp 451

RESULT 6

AA93567 ID AA93567 standard; Protein; 446 AA.

XX AA93567;

XX 25-SEP-2000 (first entry)

DE Amino acid sequence of a murine phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; murine; enzyme.

XX Mus sp.

XX EP1018559-A1.

XX 12-JUL-2000.

PF 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.
PR 17-SEP-1999; 99GB-0022123.

XX (PF12) PFIZER LTD.
XX (PF12) PFIZER INC.

PI Fldock M;

DR WPI; 2000-433274/38.

XX N-PSDB; AAA46649.

PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT useful for preventing diagnosing and treating diseases associated with
PT inappropriate PDE-XIV expression and/or activity -

PS Disclosure; Page 39-41; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC be administered to treat diseases by rectifying mutations or deletions
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

XX Sequence 446 AA;

Query Match 91.0%; Score 2192; DB 21; Length 446;
Best Local Similarity 91.6%; Pred. No. 3.5e-206;
Matches 413; Conservative 13; Mismatches 19; Indels 6; Gaps 2;

QY 1 MSCLMVERGCELLFENPDNAKVCVMIGDTRLGOTGVRAERGSYPFDIFRLNSTYTS 60
DB 1 mscImvercgevlfeexpqxxkvcvcmldgvdrltqgvgvaerqsyypfdifrlnstx 60
QY 61 GEIGTKKKVRLSFQRYFHASRLRGIIPOAPDLHLDEDDYLGOARHMLSKVGMDFDIF 120
DB 61 geigtkkkvrlsfqryfhassrlrgiipqapdlhldegylsqarhmlskvgwdtdif 120
QY 121 LFDRLTNGNSLVTLCHLFTNGLIHFKIDMYTLHREFLWVOEDYHSQNPYNAVAHAD 180
DB 121 lfdrltngnslvtllchlfntghlhfkdmytlhrfelmvoedyhsnpynavaaad 180
QY 181 VFOAMHCYLKEPKLASFLPDLIMLGILAAADVDHDPGVNOFLRTKTNHILANLVONMS 240
DB 181 vfoamhcylkepklaasflpdlimlgilaaadvdhpyvngflfktknhienlyqms 240
QY 241 VLENHHWRSTIGMLRESRLAHLPRKEMTODIEQOLSLIATDINRONEFLTRLKAHLN 300
DB 241 vlenhhwrstigmresrllahlprkemtodieqolsliatdinronefltrlkahlhn 300
QY 301 KDLRLDADNRHMLQIALKADICNPCTRIMWSKQWSEVCEFFRQGLEQKFELEIS 360
DB 301 kdrlrlexddrhmqlalalcadlcnpctrimwskqwservceeffyrqgleqkfeleis 360
QY 361 PLCNQOKDSTPSIOIGFMSYIVPELRFRENAHFNGNSTLSNMGLAHNAKQKSLPRQ 420
DB 361 plcnqokdsipsiqigfmyiveplrfrewaxftgnstlsenmlshlahnakqksslxxq 420
QY 421 HRSRGSSGSGPDHDHAGOGTESEEO-EGDSP 450

Db 421 hrrrgsg-----qdlagapapclqtegacp 446

RESULT 7

AAV93574 ID AAV93574 standard; Protein; 446 AA.

XX AAV93574;

XX 25-SEP-2000 (first entry)

XX Amino acid sequence of a phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; enzyme.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 12 /label= Val, Ile

FT Misc-difference 16 /label= Ser, Asn

FT Misc-difference 18 /label= Glu, Asp

FT Misc-difference 20 /label= Ser, Val, Asn, Ala

FT Misc-difference 21 /label= Ser, Val, Asn, Ala

FT Misc-difference 30 /label= Val, Ile

FT Misc-difference 39 /label= Pro, Arg

FT Misc-difference 56 /label= Asn, Ser

FT Misc-difference 59 /label= His, Tyr

FT Misc-difference 114 /label= Thr, Met

FT Misc-difference 141 /label= Ser, Thr

FT Misc-difference 168 /label= Gly, His, Ser, Glu

FT Misc-difference 169 /label= Gly, His, Ser, Glu

FT Misc-difference 307 /label= Asp, Ala, Asn, Val

FT Misc-difference 308 /label= Asp, Ala, Asn, Val

FT Misc-difference 350 /label= Glu, Asp

FT Misc-difference 379 /label= Ser, Thr

FT Misc-difference 391 /label= His, Arg

FT Misc-difference 404 /label= Gly, Ser

FT Misc-difference 418 /label= Pro, Arg, Ser, Asn

FT Misc-difference 419 /label= Pro, Arg, Ser, Asn

FT Misc-difference 423 /label= Ser, Arg

FT Misc-difference 430 /label= His, Leu

FT Misc-difference 433 /label= Glu, Gly, Thr, Pro, Ala

FT Misc-difference 434 /label= Glu, Gly, Thr, Pro, Ala

FT Misc-difference 435 /label= Glu, Gly, Thr, Pro, Ala

FT Misc-difference 437 /label= Ser, Glu, Thr, Leu

FT Misc-difference 438 /label= Ser, Glu, Thr, Leu
FT Misc-difference 441 /note= "optionally absent"
FT Misc-difference 444 /label= Asp, Ser, Ala, Thr
FT Misc-difference 445 /label= Asp, Ser, Ala, Thr
FT Misc-difference 445 /label= Asp, Ser, Ala, Thr
PN Epi018559-A1.

PD 12-JUL-2000.

PF 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

PA (PRIZ) PRIZER LTD.

XX (PRIZ) PRIZER INC.

DR WPI; 2000-433274/38.

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,

FT useful for preventing diagnosing and treating diseases associated with

XX inappropriate PDE-XIV expression and/or activity -

PS Disclosure: Page 70-72; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.
CC The enzyme sequence is derived from a formula of the invention. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC be administered to treat diseases by rectifying mutations or deletions
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and/or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbent assay (ELISA)).
XX Sequence 446 AA;

SQ Sequence 446 AA;

Query Match 90.0%; Score 2166; DB 21; Length 446;
Best Local Similarity 91.6%; Pred. No. 1.2e-203;
Matches 413; Conservative 0; Mismatches 32; Indels 6; Gaps 2;

QY 1 MSLWVRCGEITLFPNDONAKVCYMLGDIRLKGQGVRAERGSYPFDRLNSTYYS 60
DB 1 mslwvrcgeitlfpndonakvcymlgdirlkgqgvraergsypfdrlnstyys 60
QY 61 GEIGTKKKVKRLSFOFRFHASRLRGIIPQAPHLIDEDYLGQARHMLSKGMPDPIF 120
DB 61 geigtkkkvkrllsfqrfhnsrlrgilpqaphllidedylgqarhmlskgxvdfdf 120
QY 121 LFDRLTNGNSLYVTLLCHLFTNHGILHFRLKIDWTYLRFLYVQVEDYHSQNPYHNAVHAD 180
DB 121 lfdrltngnslyvtllchlfnthgillhfrlkidwtylrflwyvqedyhsxnpynhnaad 180
QY 181 VTQAMHCYLKPEKLASFPLDLMGLLAADVDHPGVNPFLLIKTNHMLANTYQNS 240
DB 181 vtqamhcykpeklasfpldlmglaaadvdhpgvnppflliktnhmlantyns 240

XX	OS	Homo sapiens.	
XX	FT	Key	Location/Qualifiers
XX	FT	Misc-difference	188
XX	FT	Misc-difference	/note= "Encoded by GAR"
XX	FT	Misc-difference	188
XX	FT	Misc-difference	/label= Unknown
XX	FT	Misc-difference	/note= "Encoded by CMC"
XX	FT	Misc-difference	387
XX	FT	Misc-difference	/label= Unknown
XX	FT	Misc-difference	/note= "Encoded by GNN"
XX	PN	MO200162940-A2.	
XX	XX	30-AUG-2001.	
XX	XX	20-FEB-2001; 2001MO-EP01858.	
XX	PR	21-FEB-2000; 2000EP-0103655.	
XX	PA	(MERE) MERCK PATENT GMBH.	
XX	XX	Kluxen F, Heitsch B;	
XX	XX	WPI; 2001-570636/64.	
XX	DR	N-PSDB; AAS13249.	
XX	PT	phosphodiesterase 7B proteins and nucleic acids, useful for preventing,	
XX	PT	diagnosing and treating, e.g. asthma, inflammation and allergies -	
XX	PS	Claim 1; Page 39-40; 40pp; English.	
XX	XX	The invention relates to a novel human phosphodiesterase type 7B	
XX	CC	polypeptide and the nucleic acid that encodes it. The protein and nucleic	
XX	CC	acid may be used in the prevention, diagnosis and treatment of diseases	
XX	CC	associated with inappropriate phosphodiesterase 7B (P7B) expression. For	
XX	CC	example, The protein and nucleic acid may be used to treat	
XX	CC	disorders associated with decreased expression by rectifying mutations	
XX	CC	or deletions in a patient's genome that affect the activity of P7B by	
XX	CC	expressing inactive proteins or to supplement the patient's own	
XX	CC	production of P7B. The nucleic acids may be used to produce P7B	
XX	CC	polypeptides by inserting the nucleic acids into a host cell and	
XX	CC	culturing the cell to express the protein. The nucleic acid and its	
XX	CC	complements may also be used as DNA probes in diagnostic assays to detect	
XX	CC	and quantitate the presence of similar nucleic acids in samples, and	
XX	CC	therefore which patients may be in need of restorative therapy. The P7B	
XX	CC	polypeptides may also be used as antigens in the production of it's	
XX	CC	expression and actively. The anti-P7B antibodies and antagonists may	
XX	CC	also be used to down regulate expression and activity. The anti-P7B	
XX	CC	antibodies may also be used as diagnostic agents for detecting the	
XX	CC	presence of P7B in samples (e.g. by enzyme linked immunosorbent assay	
XX	CC	(ELISA)). Disorders that may be prevented, diagnosed and/or treated by	
XX	CC	the above methods include, for example cardiovascular disease, asthma,	
XX	CC	allergy, inflammation, and immune-related disorders. The present	
XX	CC	sequence represents a human phosphodiesterase 7B.	
XX	XX	Sequence 391 AA:	

Query Match	77.5%	Score 1865;	DB 22;	Length 391;
Best Local Similarity	92.7%	Pred. No. 5.4e-174;		
Matches 354;	Conservative 2;	Mismatches 26;	Indels 0;	Gaps 0;
OY	52	RLNSTTYSGEIGCTKKRKRRLLSFQRYRPHASLLGIIIPQAPLHLDDYDYGARRHMLSK	111	
Db	10	rlnsttysgelsgltkkkrkrlisifqyrlhaslllrglllpqapllhlldedydylgqarhmlsk	69	
Y	112	VGCMDDIDFLFDRLINGNSLVTLGLCHLENTGHLIHFEKLDVMTLHRLVAVQEDYSQNP	171	

Db	70	vgmwdfidflfgrlengrnsfvtllchlfntbghllhbfkldmvtlhrflfwmgedyhaqpr	129
Qy	172	yhnnaavaavutqamscylkekrklsfplrtldimsgllaaardvuhvrgnorpflktnnn	233
Db	130	yhnaavaadvqamscylkekrklsasflrtldimgllaaardvuhvrgnqpfllktnxh	189
Qy	232	lanlyonmvsyvnlnhnrstjcmrlresrulanhrkemtovlrbqolsllandlronefl	291
Db	190	lanlyonmvsylenhbwstjgmrlresrllchlrkemtqdgldqslldadlrqnefl	249
Qy	292	trjkaillnhrkdlrledadrrhfmloialkcardicncprlwmskomservcebefrogel	351
Db	250	trjkaillnhrkdlrledagdrhfmjgialkcardicncprlwmskqswervceefrygel	309
Qy	352	eqkfefelieplrnookdsiprsioigfmsyivceulrfemahfngnstlennllghlanrka	411
Db	310	eqkfefelieplrnqgkdsiprsiqifmsyivepalrpsmahfngnstlgrtcwafanhkq	369
Qy	412	qmwslprqhrrsgsgsggprh	433
Db	370	qmwslprsteagaalaxgh	391

RESULT	12	
ID	AAV93593	
AAV93593	standard; Protein; 268 AA.	
AAV93593;		
25-SEP-2000	(first entry)	
Amino acid sequence of a human phosphodiesterase enzyme.		
Phosphodiesterase; PDE-XIV; enzyme.		
Homo sapiens.		
EP1018559-A1.		
12-JUL-2000.		
09-NOV-1999;	99EP-0308902.	
23-DEC-1998;	98GB-0028603.	
17-SEP-1999;	99GB-0022123.	
(PE12) PFIZER LTD.		
(PF12) PFIZER INC.		
Fidock M;		
WPI: 2000-433274/38.		
Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity -		
Disclosure: Page 87-88; 104pp; English.		

CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

XX Sequence 268 AA;

Query Match 59.4%; Score 1430; DB 21; Length 268;
Best Local Similarity 100.0%; Pred. No. 9.3e-132;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSCLWRECGEILFENPDQNAKVCMLGDIRLRSRGTVRAERGSYPFIDRLNSTYS 60
DB 1 mscLwreGellfEnpdqnaKvcmlgDirlrsgTvraerGsypfIdrlnStys 60
QY 61 GEIGTKKKVKRLSFQRYFHASRLRGIIPOAPLHLDEDDYLGQAHRMLSKVGMDFDIF 120
DB 61 geIgTkkKvKrlsFqRyfhAsrLrgIiPoApLhlDeeDyLgqArhMlSkvGmDfIdf 120
QY 121 LFDRLTNGNSLVTLCHLFTNTHGLIHFKLDWYTLHRLVWQEDYHSQNPYHNAVHAAD 180
DB 121 lFdrlTngNsLvTlChlFtnThglIhFkldWytLhRlVwQeDyHsqNpyHnavHaaD 180
QY 181 VTQAMHCYKLEPKLASFLPLDIMGILAAAHVDVHPCVNOPEFLIKTNHHLANLYQNS 240
DB 181 vtQamHcYlKePlKlAsFlpIdImIglIaaAahVdVhPcVnoPeFlIktnHhLanLyqNs 240
QY 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268
DB 241 vlenHhRstIgmLresrLLahlpkEmt 268

RESULT 13

AAV93568
ID AAV93568 standard; Protein; 288 AA.

AC AAV93568;

DT 25-SEP-2000 (first entry)

XX Amino acid sequence of a human phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; human; enzyme.

XX Homo sapiens.

XX EP1018559-A1.

PD 12-JUL-2000.

PF 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

PA (PFIZ) PFIZER LTD.

PA (PFIZ) PFIZER INC.

PI Fidoock M;

DR MPI: 2000-433274/38.

DR N-PSDB; AAA46650.

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
XX useful for preventing diagnosing and treating diseases associated with
XX inappropriate PDE-XIV expression and/or activity -

PS Disclosure: Page 42-44; 104pp; English.

XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The

CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC be administered to treat diseases by rectifying mutations or deletions
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e., the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

XX Sequence 288 AA;

Query Match 59.4%; Score 1430; DB 21; Length 288;
Best Local Similarity 100.0%; Pred. No. 1e-131;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSCLWRECGEILFENPDQNAKVCMLGDIRLRSRGTVRAERGSYPFIDRLNSTYS 60
DB 1 mscLwreGellfEnpdqnaKvcmlgDirlrsgTvraerGsypfIdrlnStys 60
QY 61 GEIGTKKKVKRLSFQRYFHASRLRGIIPOAPLHLDEDDYLGQAHRMLSKVGMDFDIF 120
DB 61 geIgTkkKvKrlsFqRyfhAsrLrgIiPoApLhlDeeDyLgqArhMlSkvGmDfIdf 120
QY 121 LFDRLTNGNSLVTLCHLFTNTHGLIHFKLDWYTLHRLVWQEDYHSQNPYHNAVHAAD 180
DB 121 lFdrlTngNsLvTlChlFtnThglIhFkldWytLhRlVwQeDyHsqNpyHnavHaaD 180
QY 181 VTQAMHCYKLEPKLASFLPLDIMGILAAAHVDVHPCVNOPEFLIKTNHHLANLYQNS 240
DB 181 vtQamHcYlKePlKlAsFlpIdImIglIaaAahVdVhPcVnoPeFlIktnHhLanLyqNs 240
QY 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268
DB 241 vlenHhRstIgmLresrLLahlpkEmt 268

RESULT 14

AAW00094
ID AAW00094 standard; Protein; 498 AA.

AC AAW00094;

DT 09-OCT-1996 (first entry)

XX CAMP phosphodiesterase encoded by plasmid pTM22 (ATCC 68601).

XX Human; glioblastoma cell; heat shock sensitivity; phosphodiesterase;
XX deficient yeast strain 10DBA; pTM22; rat DpD phosphodiesterase; pde1-;
XX bovine Ca2+/calmodulin dependent CAMP phosphodiesterase; heat; plasmid;
XX RAS2(val19); pde2-; pTM3; pTM72; pRATPD; pUC99; rolipram sensitive.

XX Homo sapiens.

OS US5527896-A.

PN 18-JUN-1996.

PD 20-APR-1990; 90US-0511715.

PF 19-APR-1991; 91US-0688352.

PR 20-APR-1990; 90US-0511715.

XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The

PA (COLD-) COLD SPRING HARBOR LAB.
XX Colicelli JT, Wigler MH;
XX WPI: 1996-299902/30.
DR N-PSDB; AAT34376.
XX

PI DNA mols. isolated from human glioblastoma cells - encode
XX RAS-related or cyclic nucleotide phosphodiesterase proteins
XX

PS Claim 4; Column 67-70; 101pp; English.

XX The sequences given in AAM00092-94 are encoded by plasmid fragments
CC which contain human glioblastoma cell cDNA inserts which are capable of
CC correcting the heat shock sensitivity of the phosphodiesterase
CC deficient yeast strain 10DA8. Several cDNA's were isolated and
CC sequenced. pTM22 encodes a novel human gene. From computer analysis,
CC pTM22 putatively encodes a protein homologous to various CAMP
CC phosphodiesterases, such as the bovine Ca2+/calmodulin dependent CAMP
CC phosphodiesterase and the rat DPD phosphodiesterase. Sequences related
CC to pTM22 were found to be expressed in human heart. Plasmid pTM22 was
CC unable to correct the heat shock sensitivity of RAS2(val19) yeast
CC strains. It thus appears that the pde1- and pde2- yeast strain 10DA8
CC is more sensitive to phenotypic reversion by mammalian CAMP
CC phosphodiesterase clones than is the RAS2(val19) yeast strain. The
CC inserts in the plasmids pTM3 and pTM7 were also characterized. These
CC two different CAMP phosphodiesterase cDNA's were found to be closely
CC related to, but distinct from, the PRATDP insert and the pC99 insert.
CC Biochemical analysis of cell lysates has established that the cDNA's of
CC pTM3 and pTM72, pJC44x and PRATDP encode rolipram sensitive CAMP
CC phosphodiesterases.
XX

SQ Sequence 498 AA;

Query Match 58.9%; Score 1419.5; DB 17; Length 498;
Best Local Similarity 61.7%; Pred. No. 2.5e-130;

Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

OY 7 ERCEGTELENDPDKAKVCYMLGDIRLKGOTGVRAERGSYPFIIDRLNSTTSGEIGTK 66
DB 62 qrraaisydsdqalylimlgdvrvsragfseerrgsphryidfrifhsqselewsa 121
OY 67 KKVKKLLSFQRYFNASRLNGIIPQAPRLNLDDEYLGQARNMLSKVGMDFIPLFDRLT 126
DB 122 nrlrlslsfqylrsstrfgrtavsnslnldddngqakmlekvgnmfdlfrlt 181
OY 127 NGNSLVTLCHLENTNGLIHNFKLDVTLHRFLVMVOEDYHSQNPYHNAVHADVTQAMH 186
DB 182 ngnslvslfthlfshlgleyfhlldmklrflvmiqedyhsqnpynhavhadvtqamh 241
OY 187 CYLKEPKLASFLPLDLMGLAAAHADVDHPCVNOPFLIKTNHNLANLYQMSVLENNH 246
DB 242 cylkpeklansvprwdllsliaaachldhpgvngprflfkenhylatlykxtvslenhh 301
OY 247 WRSTGMLRESRLANPKREMTODIEQGLSTLATDIRKQNEFLTRKANHANNKDLLE 306
DB 302 wrsavgllresgflshplresfsgmetqgalllatdierqeylsifshldrdgldle 361
OY 307 DAOORHMTOLAKCADICPCRIEMSKQMSRVCSEYRGCELEOKFELETSPLCNOQ 366
DB 362 dtrhrhlylqmalckadlcpcttwelskqsekveeffngldlekkyhlgvspldcrh 421
OY 367 KDSIPSTQIGFNMSTVEPLRENAHFTGNSTSENNLGLHANKAQMSKSLPRQHSRGS 426
DB 422 testaanqigimtylveplrtewarts-nrlsqmlghvglnkaskwylgqegsscdt 480
OY 427 SGS 429
DB 481 daa 483

RESULT 15

AA49808
ID AA49808 standard; Protein: 498 AA.

AC AA49808;

DT 19-JAN-2000 (first entry)

XX Human glioblastoma cell CAMP phosphodiesterase pTM22 protein.

XX Phosphodiesterase; dunce-like phosphodiesterase; pDE; DPD; CAMP;

XX RAS-related protein; immunoreactive; detection; genetic defect;

KW bronchodilation; increased myocardial contractility;

KW anti-inflammation.

OS Homo sapiens.

PN US5977305-A.

PD 02-NOV-1999.

XX 07-JUN-1995; 95US-0474379.

XX 01-MAR-1994; 94US-0206188.

PR 20-APR-1990; 90US-0511715.

PR 19-APR-1991; 91US-0688352.

XX (COLD-) COLD SPRING HARBOR LAB.

PI Colicelli JT, Wigler MH;

XX WPI: 1999-619709/73.

DR N-PSDB; AA32240.

XX New isolated RAS-related polypeptides and mammalian cyclic nucleotide

PT phosphodiesterases, used for screening for agents which can modify

XX complement or suppress genetic defects -

XX Claim 2; Column 85-88; 145pp; English.

XX The present invention describes new isolated RAS-related polypeptides
CC and mammalian cyclic nucleotide phosphodiesterases (pDES). RAS-related
CC polypeptides are capable of complementing a defective RAS function in
CC yeast. The products can be used for screening for agents which can
CC modify, complement or suppress a genetic defect in a biochemical
CC pathway in which CAMP participates, or in a biochemical pathway which
CC proteins affecting cell growth and maintenance. Developing agents that
CC will selectively act upon pDES is directed toward reproducing the
CC desirable effects of cyclic nucleotides, e.g. bronchodilation,
CC increased myocardial contractility, anti-inflammation, yet without
CC causing the undesirable effects, e.g. increased heart rate or enhanced
CC lipolysis. The products can also be used for therapeutic, diagnostic
CC and prognostic uses. AA32229 to AA32285, and AA49803 to AA49830,
CC represent sequences used in the exemplification of the present
CC invention.

SQ Sequence 498 AA;

Query Match 58.9%; Score 1419.5; DB 20; Length 498;
Best Local Similarity 61.7%; Pred. No. 2.5e-130;

Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

OY 7 ERCEGTELENDPDKAKVCYMLGDIRLKGOTGVRAERGSYPFIIDRLNSTTSGEIGTK 66
DB 62 qrraaisydsdqalylimlgdvrvsragfseerrgsphryidfrifhsqselewsa 121
OY 67 KKVKKLLSFQRYFNASRLNGIIPQAPRLNLDDEYLGQARNMLSKVGMDFIPLFDRLT 126
DB 122 nrlrlslsfqylrsstrfgrtavsnslnldddngqakmlekvgnmfdlfrlt 181
OY 127 NGNSLVTLCHLENTNGLIHNFKLDVTLHRFLVMVOEDYHSQNPYHNAVHADVTQAMH 186
DB 182 ngnslvslfthlfshlgleyfhlldmklrflvmiqedyhsqnpynhavhadvtqamh 241
OY 247 WRSTGMLRESRLANPKREMTODIEQGLSTLATDIRKQNEFLTRKANHANNKDLLE 306
DB 302 wrsavgllresgflshplresfsgmetqgalllatdierqeylsifshldrdgldle 361
OY 307 DAOORHMTOLAKCADICPCRIEMSKQMSRVCSEYRGCELEOKFELETSPLCNOQ 366
DB 362 dtrhrhlylqmalckadlcpcttwelskqsekveeffngldlekkyhlgvspldcrh 421
OY 367 KDSIPSTQIGFNMSTVEPLRENAHFTGNSTSENNLGLHANKAQMSKSLPRQHSRGS 426
DB 422 testaanqigimtylveplrtewarts-nrlsqmlghvglnkaskwylgqegsscdt 480
OY 427 SGS 429
DB 481 daa 483


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Db 182 ngnslvslfthfshlglyfhlhdmk1rrflvmiqedyhsqnp/hnavhaadvlqamh 241
QY 187 CYLKEPKLASFLPLDIMGILAAAHADVDPGVNOPFLIKTNHHLANLYONMSVLENHH 246
Db 242 cylikephiansvpwdllslaaatndidhpnqpfliktnhylatllykntsvlenhh 301
QY 247 WRSTIGMLRESRLAHLPKEMTODIEQOLSLIATDINRONEFLTRKAHLHNKDLRL 306
Db 302 wrsavglresgflshplesrqqmetqigalllatdlsrqneylsfshldrgdlcle 361
QY 307 DAODRPFMIQIALKCADICNPCKRIMENSKOMSERVCEERYROGELEOKFELEISPLCNOQ 366
Db 362 dtrhrhlvqmalckadlcpcrtwelsskqwskevteeffhgddlekkyhlyvspldcrh 421
QY 367 KDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMIGHLAHNKAOWKSILPQHRSRGS 426
Db 422 tesianigqfmylveplftewarfs-ntrlsqtmghvglnkaawkglyreqssedt 480
QY 427 SGS 429
Db 481 daa 483

```

Search completed: September 13, 2002, 12:05:28
 Job time: 344 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 12:04:54 : Search time 31.28 seconds
(without alignments)
2488.738 Million cell updates/sec

Title: US-09-471-459a-5
Perfect score: 2408
Sequence: 1 MSCLMVERGCEITFENPDQN.....PDHDAAGCTSESEQEGDSP 450

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MHC:*
- 8: SP_ORNELLAE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_PROTOZOA:*
- 12: SP_VIRUS:*
- 13: SP_VERTEBRATE:*
- 14: SP_UNCLASSIFIED:*
- 15: SP_VIRUS:*
- 16: SP_BACTERIAP:*
- 17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2252	93.5	422	4	Q9B240
2	1427.5	59.3	462	11	Q9EBR3
3	1287	53.4	424	4	Q96T72
4	603.5	25.1	803	11	Q35470
5	574.5	23.9	721	11	Q9QX17
6	573.5	23.8	542	11	Q91VY2
7	567.5	23.6	406	4	Q13945
8	565	23.5	825	4	Q9H3H2
9	562.5	23.4	518	4	Q43850
10	562	23.3	700	4	P78505
11	562	23.3	782	4	Q76105
12	562	23.3	791	4	Q43849
13	559.5	23.2	771	11	Q9BQR7
14	558.5	23.2	426	4	Q9UPJ5
15	558.5	23.2	606	4	Q9UN44
16	558.5	23.2	680	4	Q9UN45

17	558.5	23.2	712	4	Q9UN46	Q9un46 homo sapien
18	552	22.9	610	11	Q9JHQ4	Q9jHQ4 mus musculus
19	552	22.9	610	11	Q9QX48	Q9qX48 mus musculus
20	552	22.9	844	11	Q9QX49	Q9qX49 mus musculus
21	546	22.7	710	4	Q9UPJ6	Q9upJ6 homo sapien
22	517	21.5	626	5	Q95Z06	Q95z06 caenorhabdi
23	495	20.6	698	5	Q96078	Q96078 ephydralia f
24	493	20.5	624	5	Q9W4S8	Q9w4S8 drosophila
25	475	19.7	659	5	Q9NF47	Q9nf47 drosophila
26	470.5	19.5	542	11	Q9EPF9	Q9epF9 rattus norv
27	468	19.4	495	11	Q9DBS6	Q9dBS6 mus musculus
28	466	19.4	501	4	Q9C0L1	Q9c0L1 homo sapien
29	466	19.4	511	4	Q9C0K8	Q9c0K8 homo sapien
30	466	19.4	519	4	Q9UXF3	Q9uXF3 homo sapien
31	466	19.4	529	4	Q9C0L0	Q9c0L0 homo sapien
32	466	19.4	545	4	Q9C0K9	Q9c0K9 homo sapien
33	465.5	19.3	456	11	Q9JDL9	Q9jDL9 mus musculus
34	465.5	19.3	518	4	Q9C0L2	Q9c0L2 homo sapien
35	465.5	19.3	536	4	Q9C0L4	Q9c0L4 homo sapien
36	465.5	19.3	552	4	Q9C0L3	Q9c0L3 homo sapien
37	461	19.1	515	6	Q95NB8	Q95nB8 canis famli
38	461	19.1	536	6	Q9BEI6	Q9beI6 macaca fasc
39	458.5	19.0	605	5	Q9VKE9	Q9vKE9 drosophila
40	454.5	18.9	514	6	Q28063	Q28063 bos taurus
41	450.5	18.7	617	11	Q9D5W0	Q9d5W0 mus musculus
42	449	18.6	516	4	Q96KP3	Q96KP3 homo sapien
43	445.5	18.5	829	4	Q96T71	Q96T71 homo sapien
44	441.5	18.3	582	4	Q96911	Q96911 homo sapien
45	441.5	18.3	783	4	Q96PD0	Q96PD0 homo sapien

ALIGNMENTS

RESULT	ID	Q9B240	PRELIMINARY;	PRT;	422 AA.
AC	Q9B240;				
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)			
DE	BA472E5.1	(HIGH-AFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE			
DE	(EC 3.1.4.17, ROLIPRAM-INSENSITIVE PHOSPHODIESTERASE TYPE 7))				
DE	(FRAGMENT).				
GN	BA472E5.1				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
RN	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A.				
RA	Codley V.				
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AL138828; CAC27545.1; -				
DR	InterPro; IPR003607; HDC.				
DR	InterPro; IPR002073; PDase.				
DR	Pfam; PF00233; PDase; 1.				
DR	PRINTS; PR00387; PDIESTERASE1.				
DR	SMART; SM00471; HDC; 1.				
DR	PROSITE; PS00126; PDASE_1; UNKNOWN_1.				
FT	NON_TER				
FT	1				
SQ	SEQUENCE	422 AA;	48718 MW;	E5E263725119A64D CRC64;	

Query Match 93.5%; Score 2252; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 2e-190;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	29	DIRRGQTGVAAERRGSYPTDFRLNSTYSGEIGKKYKRLISORFHASRLRGI	88
DB	1	DIRRGQTGVAAERRGSYPTDFRLNSTYSGEIGKKYKRLISORFHASRLRGI	60
QY	89	IPQAPLHLDELDEYLGQARHMLSKVGMDFDIFDRRLTNGNSLVTLLCHFNTHGLTHHF	148

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Db 61 IPAPRLHDEDETLGQARHMLSKVGMDFDILFRLRNGSLVTLCHLHNTGLHNF 120
|||||
Qy 149 KLDVTLHRLVWVQEDYHSQNPYHNAVADVTQAMHCYIKERKLASFLPLDMLGL 208
|||||
Db 121 KLMVTLHRLVWVQEDYHSQNPYHNAVADVTQAMCYIKERKLASFLPLDMLGL 180
|||||
Qy 209 AAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENHMRSTIGMLRESRLAHLPKEMT 268
|||||
Db 181 AAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENHMRSTIGMLRESRLAHLPKEMT 240
|||||
Qy 269 QDIEQOGLSLTLATDINRONEFLTRLKAHLHKKDLRLDADRRHMLQIALKCADICNPC 328
|||||
Db 241 QDIEQOGLSLTLATDINRONEFLTRLKAHLHKKDLRLDADRRHMLQIALKCADICNPC 300
|||||
Qy 329 RIMEMSKOMSERVCEEFYRQGELEOKFELEISPLCNQKDSIPSIQGFMSYIPEPLFRE 388
|||||
Db 301 RIMEMSKOMSERVCEEFYRQGELEOKFELEISPLCNQKDSIPSIQGFMSYIPEPLFRE 360
|||||
Qy 389 WAHFTGNTSENMGLHLANKAOMKSLPPOHRSRSGSGSPDHADAGOTSESEBQGD 448
|||||
Db 361 WAHFTGNTSENMGLHLANKAOMKSLPPOHRSRSGSGSPDHADAGOTSESEBQGD 420
|||||
Qy 449 SP 450
1
Db 421 SP 422
1

RESULT 2
Q96RB3 PRELIMINARY: PRT: 482 AA.
ID Q96RB3
AC Q96RB3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE CAMP PHOSPHODIESTERASE 7A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX EMBL: AY007702; AAG16295.1;
RA InterPro: IPR003607; HDC.
DR Pfam: PF00233; PDase.
DR PRINTS: PR00387; PDIESTERASE1.
DR SMART: SM00471; HDC.
DR PROSITE: PS00126; PDASE_1;
SEQUENCE 482 AA: 55288 MW; E8470DD85BFF7714 CRC64;

Query Match 59.3%; Score 1427.5; DB 11: Length 482;
Best Local Similarity 62.2%; Pred. No. 14e-117;
Matches 263; Conservative 72; Mismatches 87; Indels 1; Gaps 1;

Qy 7 ERGCEILFENPDONAKVCMLGDRLRGOTGVRAERGSYFPIIDRLINSTYSGEIGTK 66
|||||
Db 46 QRGALSYDSDDTALYIRMLGDVRYVRSGAGSESESRSHYIDRIFHSOSEIEVSVA 105
|||||
Qy 67 KKVRRLLSFQRYFFHARLLRGITIPAPRLHLDDEDETLGQARHMLSKVGMDFDILFDRLT 126
|||||
Db 106 RNIIRLLSFQRYFFHARLLRGITIPAPRLHLDDEDETLGQARHMLSKVGMDFDILFDRLT 165
|||||
Qy 127 NGNSLVTLCHLHNTGLHNFHKKLDVTLHRLVWVQEDYHSQNPYHNAVADVTQAMH 166
|||||
Db 166 NGNSLVTLCHLHNTGLHNFHKKLDVTLHRLVWVQEDYHSQNPYHNAVADVTQAMH 225
|||||
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Qy 187 CYLKEPKLASFLPLDMLGLAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENH 246
|||||
Db 226 CYLKEPKLASFLPLDMLGLAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENH 285
|||||
Qy 247 WRSTIGMLRESRLAHLPKEMTQDIEQOGLSLTLATDINRONEFLTRLKAHLHKKDLRL 306
|||||
Db 286 WRSAVGLLRSGFLSHLPLESRQMEAOIGALITATDISRONEYLSLFRSHLDGDLHL 345
|||||
Qy 307 DAODRHFMLOIALKCADICNPCRIMEMSKOMSERVCEEFYRQGELEOKFELEISPLCNQ 366
|||||
Db 346 DGRHHIVLQWALIKCADICNPCRNMELSKOMSEKVTSEFFHOGDIKKYHLGVSPLCDRQ 405
|||||
Qy 367 KDSIPSIQGFMSYIPEPLFREWAHFTGNTSENMGLHLANKAOMKSLPPOHRSRGS 426
|||||
Db 406 TESTIANIQGFMTYLVPEPLTEWARRS-DTRLSQFVLGHVGLKASWVGLORQPSSEDA 464
|||||
Qy 427 SGS 429
1
Db 465 NAA 467
1

RESULT 3
Q96T72 PRELIMINARY: PRT: 424 AA.
ID Q96T72
AC Q96T72;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE CAMP-SPECIFIC CYCLIC NUCLEOTIDE PHOSPHODIESTERASE PDE7A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX EMBL: AF332652; AAK57640.1;
RA "T cell activation up-regulates cyclic nucleotide phosphodiesterases
8A1 and 7A3."
RT Proc. Natl. Acad. Sci. U.S.A. 98:6319-6324(2001).
DR EMBL: AF332652; AAK57640.1;
SEQUENCE 424 AA: 48827 MW; A7DBP40D08A7B561 CRC64;
```

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Query Match 53.4%; Score 1287; DB 4: Length 424;
Best Local Similarity 62.7%; Pred. No. 2.9e-105;
Matches 235; Conservative 64; Mismatches 76; Indels 0; Gaps 0;

Qy 7 ERGCEILFENPDONAKVCMLGDRLRGOTGVRAERGSYFPIIDRLINSTYSGEIGTK 66
|||||
Db 46 QRGALSYDSDDTALYIRMLGDVRYVRSGAGSESESRSHYIDRIFHSOSEIEVSVA 105
|||||
Qy 67 KKVRRLLSFQRYFFHARLLRGITIPAPRLHLDDEDETLGQARHMLSKVGMDFDILFDRLT 126
|||||
Db 106 RNIIRLLSFQRYFFHARLLRGITIPAPRLHLDDEDETLGQARHMLSKVGMDFDILFDRLT 165
|||||
Qy 127 NGNSLVTLCHLHNTGLHNFHKKLDVTLHRLVWVQEDYHSQNPYHNAVADVTQAMH 166
|||||
Db 166 NGNSLVTLCHLHNTGLHNFHKKLDVTLHRLVWVQEDYHSQNPYHNAVADVTQAMH 225
|||||
Qy 187 CYLKEPKLASFLPLDMLGLAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENH 246
|||||
Db 226 CYLKEPKLASFLPLDMLGLAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENH 285
|||||
Qy 247 WRSTIGMLRESRLAHLPKEMTQDIEQOGLSLTLATDINRONEFLTRLKAHLHKKDLRL 306
|||||
Db 286 WRSAVGLLRSGFLSHLPLESRQMEAOIGALITATDISRONEYLSLFRSHLDGDLHL 345
|||||
Qy 307 DAODRHFMLOIALKCADICNPCRIMEMSKOMSERVCEEFYRQGELEOKFELEISPLCNQ 366
|||||
Db 346 DTRHRHIVLQWALIKCADICNPCRTWELSKOMSEKVTSEFFHOGDIKKYHLGVSPLCDRH 405
|||||
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QY      367 KDSIPSIQIGFMSYI 381
        :||:|||| |:|
Db      406 TESIANIQIGNYYTL 420
```

RESULT	4			
035470				
ID	035470	PRELIMINARY;	PRT;	803 AA.
AC	035470;			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	CAMP-SPECIFIC PHOSPHODIESTERASE.			
GN	PDE4D.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY;			
RA	Jin S.-L.C., Kuo W.-P., Conti M.;			
RT	"Characterization of a camp-specific phosphodiesterase variant (PDE4D) expressed in the rat brain."			
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF031373; AAB95266.1; -			
DR	InterPro: IPR003607; HDC.			
DR	InterPro: IPR002073; PDEase.			
DR	Pfam: PF00233; PDEase: 1.			
DR	PRINTS: PR00387; PDIESPRASEL.			
DR	SMART: SM00471; HDC: 1			
DR	PROSITE: PS00126; PDEASE_1; 1.			
QO	SEQUENCE 803 AA; 90552 MW; 13E28B257556496D CRC64;			

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DF 01-OCW-2000 (TREMBLrel_15, Last sequence update)
DE 01-JUN-2001 (TREMBLrel_11, Last annotation update)
DI CAMP-SPECIFIC PHOSPHODIESTERASE 4B, CAMP
DE SPECIFIC).
GN PDE4B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090.
RN [1]
RP .SEQUENCE FROM N.A.
RC STRAIN-SWISS WEBSTER;
RA Cherry J.A., Thompson B.E., Pho V.;
RT "Cloning and biochemical characterization of cyclic AMP
RT phosphodiesterase isoforms in the mouse."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP .SEQUENCE FROM N.A.
RC STRAIN-SWISS WEBSTER;
RA Cherry J.A., Thompson B.E., Pho V.;
RT "Diazepam and rolipram differentially inhibit CAMP-specific
RT phosphodiesterases, PDE4A1 and PDE4B3 in the mouse."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF208023; AAF19202.2; -
DR EMBL; AJ297397; CAB96770.1; -.
DR MGD; MGI:99557; Pde4b.
DR InterPro; IPR003607; HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase.1.
DR PRINTS; PRC0387; PDE5ERRASEL.
DR SMART; SM00471; HDC.1..
DR PROSITE; PS00126; PDEASE_L; 1.
SQ SEQUENCE 721 AA; 82074 MW; 302311CA44636E7F CRC64;

```

RESULT	5	
Q9QXI7		
ID	Q9QXI7	PRELIMINARY;
AC	Q9QXI7;	PRT; 721 AA
DT	01-MAY-2000	(TREMblrel, 13, Created)

RESULT	6	
Q91VY2		
ID	Q91VY2	PRELIMINARY;
AC	Q91VY2;	PRT; 542 AA
DT	01-DEC-2001	(TREMBLrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE SIMILAR TO PHOSPHODIESTERASE 4B, CAMP-SPECIFIC (DUNGE
 DE (DROSOPHILA)-HOMOLOG PHOSPHODIESTERASE E4) (FRAGMENT).
 OS Mus musculus (mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BREAST TUMOR;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC007155; AAH07155.1; .
 FT NON_TER 1 1
 SO SEQUENCE 542 AA; 62279 MW; 886296DA16275B34 CRC64;

Query Match 23.8%; Score 573.5; DB 11; Length 542;
 Best Local Similarity 31.9%; Pred. No. 3,7e-42;
 Matches 129; Conservative 91; Mismatches 158; Indels 27; Gaps 7;

QY 66 KKKVKRLS---FQRYFNASRLRGITPOAPHLHLDDEYLGQARRHLSKYGMDFDIFL 121
 DB 104 KKKKQOLMTQISGVYKLLHSSSLNNTSISRGVNTENEDHLAKLEDLNR--WGLNIFN 160
 QY 122 FDLRTNGNSLVTLCHLFNTHGLIHFKLDVYTLHFLVWQEDYHSQNPYHNAVHADV 181
 DB 161 VAGYSNRPRLTICMVAIFQERDLTKFKISSDFEYTKMTEDEHYHSDVAYHNSLHAADV 220
 QY 182 TOAMHCYLKEPKLASFPLPDIMGLLAAAHVDHPGVNOFPLIKTHHNLANLYOMNSV 241
 DB 221 AOSTHYLLSPALDAVFTDLEILAIIPAALIHVDHPGVSNQPLINTSELALMYNDESV 280
 QY 242 LENHWRSTIGMLRESR--LLAHLPKEMTODIEQOLSLATDINONEFLTRKANH 299
 DB 281 LENHHLAVGFKLQEHHCDFQNLTKKORQTLRKAVIDMYLATDMSKHSMLDLAKTWVE 340
 QY 300 NKD-----LRLEDQDRHFMQLATLKCADICNPCRITWMSKQSEVCEEFYRQGELEQ 353
 DB 341 TKKVTSSGVLLDNDYTRIQVLRNMYHGCADLSNPKLSLELRQMTDIMEEFPQGDKEK 400
 QY 354 KFELEISPLCNOQKDSIPSIQIGFMSYIYEPLEFRAWHTGNSLTSENNLGHLANHAKQW 413
 DB 401 ERGMEISPMCDKHTASVKSQVGFIDYIVHPLMETWADLVQPD--ADLDLTLEDNRNMY 458
 QY 414 KSLLPK-----QHRSGSSGSGPDH-----AGQTESEDEQD 448
 DB 459 QSMTPQSPPLDERSRDCQGLMEKFOFELTLDEEDSEKPEKEG 503

RESULT 7
 ID 013945 PRELIMINARY; PRY; 606 AA.
 AC 013945;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE 3,5'-CYCLIC AMP PHOSPHODIESTERASE (FRAGMENT).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=93314968; PubMed=8392015;
 RA Oberholte R., Bhakta S., Alvarez R., Bach C., Mulkins M., Jarnagin K.,
 RA Shelton E.R.;
 RT "The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV)
 RT reveals a multigene family.";
 RL Gene 129:239-247(1993).
 DR EMBL: L12686; AAA35643.1; .
 DR InterPro: IPR003607; HDC.

DR InterPro: IPR002073; PDEase.
 DR Pfam: PR00233; PDEase; 1
 DR PRINTS: PR00387; PDIESTERASEL.
 DR SMART: SM00471; HDC; 1
 DR PROSITE: PS00126; PDEASE_I; 1.
 KW CAMP.
 FT NON_TER 1 1
 SO SEQUENCE 606 AA; 68663 MW; 256BD63B32C79398 CRC64;

Query Match 23.6%; Score 567.5; DB 4; Length 606;
 Best Local Similarity 31.3%; Pred. No. 1.4e-41;
 Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;

QY 66 KKKVKRLS---FQRYFNASRLRGITPOAPHLHLDDEYLGQARRHLSKYGMDFDIFL 121
 DB 168 KKKKQOLMTQISGVYKLLHSSSLNNTSISRGVNTENEDHLAKLEDLNR--WGLNIFN 224
 QY 122 FDLRTNGNSLVTLCHLFNTHGLIHFKLDVYTLHFLVWQEDYHSQNPYHNAVHADV 181
 DB 225 VAGYSNRPRLTICMVAIFQERDLTKFKISSDFEYTKMTEDEHYHSDVAYHNSLHAADV 284
 QY 182 TOAMHCYLKEPKLASFPLPDIMGLLAAAHVDHPGVNOFPLIKTHHNLANLYOMNSV 241
 DB 285 AOSTHYLLSPALDAVFTDLEILAIIPAALIHVDHPGVSNQPLINTSELALMYNDESV 344
 QY 242 LENHWRSTIGMLRESR--LLAHLPKEMTODIEQOLSLATDINONEFLTRKANH 299
 DB 345 LENHHLAVGFKLQEHHCDFQNLTKKORQTLRKAVIDMYLATDMSKHSMLDLAKTWVE 404
 QY 300 NKD-----LRLEDQDRHFMQLATLKCADICNPCRITWMSKQSEVCEEFYRQGELEQ 353
 DB 405 TKKVTSSGVLLDNDYTRIQVLRNMYHGCADLSNPKLSLELRQMTDIMEEFPQGDKEK 464
 QY 354 KFELEISPLCNOQKDSIPSIQIGFMSYIYEPLEFRAWHTGNSLTSENNLGHLANHAKQW 413
 DB 465 ERGMEISPMCDKHTASVKSQVGFIDYIVHPLMETWADLVQPD--ADLDLTLEDNRNMY 522
 QY 414 KSLLPKQHRSGSSGSGP-----DHDHNG-----QGTSEDEQD 448
 DB 523 QSMTPQ-----SPSPLEDRNDCQGLMEKFOFELTLDEEDSEKPEKEG 567

RESULT 8
 ID 09H3H2 PRELIMINARY; PRY; 825 AA.
 AC 09H3H2;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CYCLIC AMP-SPECIFIC PHOSPHODIESTERASE HSPDEA10.
 GN PDE4A.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA Rena G., Begg F., Ross A., Mackenzie C., McPhee I., Campbell I.,
 RA Huston E., Sullivan M., Houslay M.D.;
 RT "Molecular cloning, genomic positioning, promoter identification and
 RT characterisation of the novel CAMP-specific phosphodiesterase,
 RT PDE4A10.";
 RL Mol. Pharmacol. 0:0-0(2001).
 DR EMBL: AF073745; AAD34217.2; .
 DR InterPro: IPR003607; HDC.
 DR InterPro: IPR002073; PDEase.
 DR Pfam: PR00233; PDEase; 1.
 DR PRINTS: PR00387; PDIESTERASEL.
 DR SMART: SM00471; HDC; 1
 DR PROSITE: PS00126; PDEASE_I; 1.
 SO SEQUENCE 825 AA; 91322 MW; B50A342801E605FB CRC64;

SO SEQUENCE 700 AA; 77600 MW; B39732360C2E18A5 CRC64;

Query Match	23.3%	Score 562;	DB 4;	Length 700;
Best Local Similarity	28.2%;	Pred. No. 5.3e-41;		
Matches 137;	Conservative 92;	Mismatches 198;	Indels 58;	Gaps 10;

OY 11 EEFENDONAKOVCLGIRLRAGOTGVARRRGSGYPFIDRLIN-----STYSG-- 61
 Db 192 KIALFTLDELDMCLODLQLETLOTQRHSVGEAMANKPK-----RLINRELTHLSETSRGNO 241
 OY 62 -----ELGTGR-----KVRLLSPORFYHAARLLRGLIPAPLHLIDE 99
 Db 246 VSEIKSRFLDOOTVEELRKVAEAPQPMRSIGLIGLHSHASLSASATVPFRGVOITDE 301
 OY 100 DYLCQARHMLSKKGMDFEIPFEDRLTNGSLVTLVLCHELFNFGILLHNKRLLMVTLHRL 15
 Db 306 EOLAKE---LEDYNNKKGDLVFYKVALSLGNOPLTGIIIFSIOERBLTKTQDIPADLTATL 36
 OY 160 VMVQEDHSQNPYHNVAHADVTQOMCHCYLKEPKIASFLPRLDIMGLLAAAANDVDHG 21
 Db 363 LMLGCHHANAVANHSLHAAVDAOSTHVLATPRLVLEAVFTDLELIALFASAHVDVHG 42
 OY 220 VNOEFLTKTNNHLANLYOMASVLENNHRSYIGMLRESR--LLAHLKRENTODIEOLGS 27
 Db 423 VSNQFLINTNSEALMYNDSVLENNHHLAVGFKLLOAENCDFIIONLSAKRSLRKMVID 48
 OY 278 LILATDINRQNEFLTRIKKHLHNK-----LRLEDADRHFMQLQALKICNCRIM 33
 Db 483 MVLATDMSKHNHLADLKIMVETKRYVSLGYLLLDNVSDRLOYLQNLVHCAADLSNPTKL 54
 OY 332 EMSQMSBRVCEEFYRQGLEOKFELETSPLCNQOKDSIPISQIGFMSYIVLEPRFMAH 39
 Db 543 PLYRQWTDRLMAEFQOQGRERESGIDTSPMDKRTAASVEKSGYGLDYIAHPLMETAD 60
 OY 392 FTGNSITSENNLGLLHNKAKWMSLLPROHRS-RGSSGSGDH-----DHAGQGTSEB 44
 Db 603 LVHPD--AODLLDTLEDNREMYOSKIPRSPSLDINPERDGPDRFOFELTLEAEBEEDBE 66
 OY 444 EOEGD 448 : : : : :
 Db 661 EEEGE 665 : : : : :
 RESULT 11
 OY 076105 PRELIMINARY; PRT: 782 AA.
 AC 076105
 DT 01-NOV-1998 (TREMBLrel, 08, Created)
 DT 01-NOV-1998 (TREMBLrel, 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel, 19, Last annotation update)
 DE PDEAC-791 (FRAGMENT).
 GN PDEAC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId:9606;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP Lamerdin J.E., McCreedy P.M., Skowronski E., Wiswanathan V.,
 RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez G., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Davies J., Avila J.,
 RA Danganan L., Poundstone P., Christensen M., Georgescu I.,
 RA Liu S., Altix C., Andreise T., Frankheim M., Amico-Keller G.,
 RA Coetfield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
 RA Krombailier B., Arellano A., Saunders C., Ow D., Nolan M., Truong S.,
 RA Kobayashi A., Olsen A.S., Carraro A.V.;
 RT "Sequence analysis of an ~600 kb region in 19p13.1 between JAK3 and
 RL PDEAC".
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC000575; AAC83050.1; -
 DR InterPro: IPR003607; HBC
 DR InterPro: IPR002073; PDBase.

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DR      pfam; PF00233; PDEase; 1.
DR      PRINTS; PR00387; PDIESTERASE1.
DR      SMART; SM00471; HDC; 1.
DR      PROSITE; PS00126; PDEASE_I; 1.
DR      SMART; SM00471; HDC; 1.
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Query Match	23.3%;	Score 562;	DB 4;	Length 782;
Best Local Similarity	28.2%;	Pred. No. 6.2e-41;		
Matches 137; Conservative	92;	Mismatches 198;	Indels 58;	Gaps 10;

OY		.1	ELEPHENDONAKKOCVMIIGDRIIRLNGOTGVABERKSVPFIDRLN-----STTSG--	61
Dd		274	KIALETIDEIDMCLDOLETLQTRHSGVEMASKFK-----RILNRETLHSETSRSGNQ	327
OY		62	-----EIGTK-----KVRRLSFORFYFNASRLNRGIIPOAPLHLDE	99
Dd		328	VSEYISFTLDQOEVELRPVTUEAPROPMSRSISGLHCISASLSATVPBFGVOTDQE	387
OY		100	DYICQAHMYLSKYCMWPFEDFLDRLTNNSLVTLICHIFENHGCHINHFCKIDMTYLHRFL	159
Dd		388	EQLAKE---LEDTPKKWGLDVFVKVAELSGNRPLTAIIFSIOBERDLTKFFOIPADTLATYL	444
OY		160	VWNOEDHYSONPNNVANNADYQAANIKYLEKEKIASFTLPDIIMIGLAAAADVDVDPG	219
Dd		445	LMLEBHNIANAAYINSIHADAVQSHVLALPRALEAVPTDELIALAFAAISIHVDVHPG	504
OY		220	VNOPRLKTNHNLANKVNNSVLENHHNMSTOMLEERS--LLAALPREMODIEOOLGS	277
Dd		505	VSNOPRLITNSELAMYNDSASVLENNHNAVGFLLQAEKCDFIFOYLSAKORLSLRRAVID	564
OY		278	LIALDIRKQHEFLTRLKAHLHNKD-----LEDEAOBRPMLOIAKCAIDINPCRIW	331
Dd		565	NWLADMKRNHNLADLKTVETRKVTSGLVILLDNYSDRIGOVLNIVHCADLSENPKPL	624
OY		332	BMSKOMSRVOEEFRYGEGELEOKFEELISPLCQOOKDSIPSIQIFESVYEPLFREMAN	391
Dd		625	PXYRWOTRIMAEEFOQODRESGLDISPMCDKHRTASYEKSOVGFIYIAHPIMETWAD	684
OY		392	FPGNSTLESNNIGHLANHKOWKSLRPROHS--RGSSGGSPDH-----DHAGCGESE	443
Dd		685	LVNHPD--AQDDLOTLEDREHYOSKIRPSRSDLTNPERGDPRQFELLLEEAREEDEEE	742
OY		444	EOEGD 448	
Dd		743	EEEGE 747	
RESULT	12			
ID	043849	PRELIMINARY;	PRT; 791 AA.	
AC	043849:			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)			
Dd	PDBEC-791 (PDB4C-426) (FRAGMENT).			
GN	EDECAC			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_Taxid=9606;			
RX	111			
RC	SEQUENCE FROM N.A.			
RP	TISSUE-TESTIS;			
RX	MEDLINE=95145731. Pubmed-7843419;			
RA	Beggs J P., Sullivan M., Muller T., Lubbert H.;			
RT	Molecular cloning and functional expression in yeast of a human cAMP-			
RT	specific phosphodiesterase subtype (PDE IV-C).";			
RL	PNAS Lett. 358:305-310(1995).			
RL	121			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-TESTIS, AND LUNG;			

RX MEDLINE=98007880; PubMed=9349724;
 RA Jernagin R., Ratzliff J., Baecker P.A., Daniels D.V., Zuppan P.,
 RA Jernagin K., Shelton E.R.;
 RT "Multiple splice variants of phosphodiesterase PDE4C cloned from human
 RT lung and testis";
 RL Biochim. Biophys. Acta 1353:287-297(1997).
 DR EMBL; U66346; AAB96875.1; -;
 DR EMBL; U66347; AAB96876.1; -;
 DR Interpro: IPR003607; HDC.
 DR Interpro: IPR002073; PDEase.
 DR Pfam: PF00233; PDEase; 1.
 DR PRINTS; PR00387; PDIESTERASE1.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 FT NON_TER 1 1
 FT SEQUENCE 791 AA; 88142 MW; 616F606E39719B8 CRC64;

Query Match 23.3%; Score 562; DB 4; Length 791;
 Best Local Similarity 28.2%; Pred. No. 6.3e-41;
 Matches 137; Conservative 92; Mismatches 198; Indels 58; Gaps 10;

QY 11 EILENDQNAKCYCMGDIPLRGQGYRAERGSYPIIDRLN-----STTYSG-- 61
 DB 283 KIALETIDELDMCIDOLETQTRHSVGEAMSNKPK-----RIINRELTHLSETSRSGNQ 336
 QY 62 -----EIGTKK-----KYKRLSFQRYPHASRLGLIIPQAPLHLDE 99
 DB 337 VSEIISTRLDQOTEVLEPKYTAEEAPQPMKRISGLHGLCHSASLSATVYRFGVQDOE 396
 QY 100 DYLGQARHMLSKVGMDFEFLFDRLTNGNSLVTLCHLFNTHGLIHNFKLDWVTLHREFL 159
 DB 397 EOLAKE---LEDTKMGKGLDVKVAELSGNQLTAIFSIQFERDLTKTFOIPADTLATYL 453
 QY 160 VMQVEDHSQPRYNNAHAADVYQAMHCYLERKLASFLPLDLMIGLLAAAHADVHPG 219
 DB 454 LMLGHHYANVAHNSHAAVQASTHYLLATPALAEVFDLETLAALFASAIHDVHPG 513
 QY 220 VNQFPLKTNHNLNQNMSVLENHHRSTIGMLRESR--LLAHLPRKEMQDIEQOLGS 277
 DB 514 VSNQFPLINTNSLALMNDASVLENHHLAVGFKLQAEKNCIFQNLASKQKSLRMYID 573
 QY 278 LIALTDINRQNEFLTRKLAHLNKKD-----LRLEDAODRHFMQIALKADICNPCRIM 331
 DB 574 MVLATDMSKHNMLADLKTWETKKVTSIGVLLDNDYSDRQVLRNMYHCAADLSNPKPL 633
 QY 332 EMSQWSEVCEEFYRQGELEQKFELEISPLCNOQKDSIPSIQIGFMSYIEPLREMAH 391
 DB 634 PLYRQWTDRIAEFFQOGDRERESGLDISPMCDKHTASVEKSYGFIIDYIHPMETWAD 693
 QY 392 FTGNTSTSENNLGLHANNAKQWKSLLPRQHS-RGSSSGSGPDH-----DHAGOGTSE 443
 DB 694 LVHPD--AQDILDTLEDNRKRWYQSKIRPSDGLTNPERRQDPQFELTLEAEEDDEE 751
 QY 444 EOEGD 448
 DB 752 EEEDG 756
 RESULT 13
 Q9EOR7 PRELIMINARY; PRT; 771 AA.
 AC Q9EOR7;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CYCLIC AMP PHOSPHODIESTERASE PDE4A10 (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Rena G., Begg F., Ross A., Mackenzie C., McPhee I., Campbell L.,
 RA Huston E., Sullivan M., Houslay M.D.;
 RT "Molecular cloning, genomic positioning, promoter identification and
 RT characterisation of the novel cAMP-specific phosphodiesterase,
 RT PDE4A10";
 RL Mol. Pharmacol. 0:0-0(2001).
 DR EMBL; AF110461; AAF14352.2; -;
 DR Interpro: IPR003607; HDC.
 DR Interpro: IPR002073; PDEase.
 DR Pfam: PF00233; PDEase; 1.
 DR PRINTS; PR00387; PDIESTERASE1.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 FT NON_TER 1 1
 FT SEQUENCE 771 AA; 85459 MW; D20712E515CDAFOB CRC64;

Query Match 23.2%; Score 559.5; DB 11; Length 771;
 Best Local Similarity 31.1%; Pred. No. 1e-40;
 Matches 133; Conservative 77; Mismatches 163; Indels 55; Gaps 9;

QY 43 RGSYPIIDRLNNTTSGELGTTKKYKRLLSFQRYPHASRLGLIIPQAPLHLDEYL 102
 DB 241 RQSPMSQITGLKRLVHTGSLNTN-----VRFVSKTDQEDLL 278
 QY 103 GQARHMLSKVGMDFEFLFDRLTNGNSLVTLCHLFNTHGLIHNFKLDWVTLHREFLMV 162
 DB 279 AQELEENK---KGLNIFCVSEYAGNSLSCTMTTIFQERDLKKFHPVITMMYMLTL 335
 QY 163 QEDYHSQPRYNNAHAADVYQAMHCYLERKLASFLPLDLMIGLLAAAHADVHPGVNQ 222
 DB 336 EDHYADVAHNSHAAVQASTHYLLATPALDAVFTDLTALFPAAIHDVHPGVS 395
 QY 223 PFLKTNHNLNQNMSVLENHHRSTIGMLRESR--LLAHLPRKEMQDIEQOLGSLIL 280
 DB 396 QFLINTNSLALMNDASVLENHHLAVGFKLQAEKNCIFQNLASKQKSLRMYIDMV 455
 QY 281 ATDINRQNEFLTRKLAHLNKKD-----LRLEDAODRHFMQIALKADICNPCRIMWS 334
 DB 456 ATDMSKHNMLADLKTWETKKVTSIGVLLDNDYSDRQVLRNMYHCAADLSNPKPL 515
 QY 335 KQWSEVCEEFYRQGELEQKFELEISPLCNOQKDSIPSIQIGFMSYIEPLREMAHFTG 394
 DB 516 RQWTDRIAEFFQOGDRERESGLDISPMCDKHTASVEKSYGFIIDYIHPMETWADLVH 575
 QY 395 NSTSENNLGLHANNAKQWKSLLPRQHSRGSSSGP-DHHAOG-----TE 441
 DB 576 PD--AQDILDTLEDNR-DW-----YHSAIRQSPSPLEERPGIGHPSLPKQFELTL 626
 QY 442 SEEDG 449
 DB 627 EEEEDS 634
 RESULT 14
 Q9UPJ5 PRELIMINARY; PRT; 426 AA.
 AC Q9UPJ5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE PDE4C-426.
 GN PDE4C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J.,

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 12:02:04 ; Search time 20.91 Seconds
(without alignments)
2067.920 Million cell updates/sec

Title: US-09-471-459a-5

Perfect score: 2408

Sequence: 1 MSLWVRCRGCELLFENPDQN.....PDHDAQGQGTSESEQESDSP 450

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2408	100.0	450	2 JC7266	3',5'-cyclic-nucle
2	1419.5	58.9	498	2 A47286	3',5'-cyclic-AMP p
3	604.5	25.1	673	2 B16358	3',5'-cyclic-nucle
4	603.5	25.1	584	2 B53109	3',5'-cyclic-nucle
5	580.5	25.1	672	2 B16259	3',5'-cyclic-nucle
6	580.5	24.1	562	2 I59143	CAMP phosphodiesterase
7	580.5	24.1	564	2 A40949	cyclic-AMP phospho
8	567.5	23.6	564	2 JC1519	3',5'-cyclic-nucle
9	567.5	23.6	736	2 B16354	phosphodiesterase
10	565	23.5	886	2 A54442	3',5'-cyclic-nucle
11	559.5	23.2	610	2 B16946	3',5'-cyclic-nucle
12	559.5	23.2	610	2 I53865	phosphodiesterase
13	553	23.0	712	2 S71626	3',5'-cyclic-nucle
14	529.5	22.0	536	2 I67945	3',5'-cyclic-nucle
15	517	21.5	549	2 T16769	hypothetical prote
16	493	20.5	777	2 S65543	3',5'-cyclic-nucle
17	477.5	19.8	323	2 S55348	3',5'-cyclic-nucle
18	468	19.4	267	2 B33904	CAMP phosphodiesterase
19	468	19.4	535	1 A46378	3',5'-cyclic-nucle
20	467	19.4	534	1 A44162	3',5'-cyclic-nucle
21	466	19.4	519	2 T14783	hypothetical prote
22	466	19.4	535	1 A44161	3',5'-cyclic-nucle
23	461	19.1	664	2 T24459	hypothetical prote
24	454.5	18.9	530	1 A45334	3',5'-cyclic-nucle
25	452.5	18.8	768	2 T10796	3',5'-cyclic-nucle
26	449	18.5	536	1 JC6129	3',5'-cyclic-nucle
27	445.5	18.5	713	2 JH0088	3',5'-cyclic-nucle
28	441	18.3	659	2 JH0293	3',5'-cyclic-nucle
29	409	17.0	491	2 A40283	3',5'-cyclic-nucle

30	381	15.8	875	1 JH0106	3',5'-cyclic-GMP p
31	377	15.7	875	1 A48719	3',5'-cyclic-GMP p
32	370	15.4	1054	2 T30901	cyclic nucleotide
33	368.5	15.3	1112	2 S70522	cyclic nucleotide
34	357.5	14.8	1108	2 A48508	cyclic nucleotide
35	346	14.4	1141	2 A44093	cGMP-inhibited cAMP
36	302.5	12.6	858	2 JC4520	3',5'-cyclic-GMP p
37	300	12.5	855	2 A34810	3',5'-cyclic-GMP p
38	299	12.4	928	1 JC2486	3',5'-cyclic-nucle
39	296	12.3	921	1 A40981	3',5'-cyclic-nucle
40	283	11.8	853	2 A36617	3',5'-cyclic-GMP p
41	279	11.6	856	1 A47451	3',5'-cyclic-GMP p
42	278	11.5	856	2 S30762	3',5'-cyclic-GMP p
43	277.5	11.5	854	2 A42828	3',5'-cyclic-GMP p
44	269.5	11.2	862	2 I50186	3',5'-cyclic-GMP p
45	268	11.1	859	2 B34611	3',5'-cyclic-GMP p

ALIGNMENTS

RESULT 1	
JC7266	
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 7B - human	
N:Alternate names: CAMP-specific phosphodiesterase 7B	
C:Species: Homo sapiens (man)	
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000	
C:Accession: JC7266	
R:Sasaki, T.; Kotera, J.; Yusa, K.; Omori, K.	
Biochem. Biophys. Res. Commun. 271, 575-583, 2000	
A>Title: Identification of human PDE7B, a CAMP-specific phosphodiesterase.	
A:Reference number: JC7266	
A:Accession: JC7266	
A:Molecule type: mRNA	
A:Residues: 1-450 <SAS>	
A:Cross-references: DDBJ:AB038040	
A:Experimental source: caudate nucleus	
C:Genetics:	
A:Gene: pde7B	
A:Map position: 6q23-24	
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3'	
C:Keywords: phosphoric diester hydrolase	
Query Match	100.0%; Score 2408; DB 2; Length 450;
Best Local Similarity	100.0%; Pred. No. 1.2e-183;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MSLWVRCRGCELLFENPDQNAKVCMLGDIRLGGTGVRAERGSYPFLDFRLNSTYS 60	
1 MSLWVRCRGCELLFENPDQNAKVCMLGDIRLGGTGVRAERGSYPFLDFRLNSTYS 60	
QY 61 GEIGTKKKVRLISFQRYHNASRLRGITPQAPLHLLDEDDYLGQARNHLSKGMDFDIF 120	
61 GEIGTKKKVRLISFQRYHNASRLRGITPQAPLHLLDEDDYLGQARNHLSKGMDFDIF 120	
QY 61 GEIGTKKKVRLISFQRYHNASRLRGITPQAPLHLLDEDDYLGQARNHLSKGMDFDIF 120	
61 GEIGTKKKVRLISFQRYHNASRLRGITPQAPLHLLDEDDYLGQARNHLSKGMDFDIF 120	
QY 121 LFDRLNGNSLVTLGHLNFTGHLHHFKLDVTLRLFLVMOVEDYHSONPYNAVAHAD 180	
121 LFDRLNGNSLVTLGHLNFTGHLHHFKLDVTLRLFLVMOVEDYHSONPYNAVAHAD 180	
QY 121 LFDRLNGNSLVTLGHLNFTGHLHHFKLDVTLRLFLVMOVEDYHSONPYNAVAHAD 180	
121 LFDRLNGNSLVTLGHLNFTGHLHHFKLDVTLRLFLVMOVEDYHSONPYNAVAHAD 180	
QY 181 VTQAMHCYKEPKLASFLPLDIMGILAAAHVDHPCVNOPEFLTKTNHNLANTYONNS 240	
181 VTQAMHCYKEPKLASFLPLDIMGILAAAHVDHPCVNOPEFLTKTNHNLANTYONNS 240	
QY 181 VTQAMHCYKEPKLASFLPLDIMGILAAAHVDHPCVNOPEFLTKTNHNLANTYONNS 240	
181 VTQAMHCYKEPKLASFLPLDIMGILAAAHVDHPCVNOPEFLTKTNHNLANTYONNS 240	
QY 241 VLENHNRSTIGMLRSRLLAHLPKEMTODIEQOLGSLIADDDINQNEFLRLKAKHLN 300	
241 VLENHNRSTIGMLRSRLLAHLPKEMTODIEQOLGSLIADDDINQNEFLRLKAKHLN 300	
QY 241 VLENHNRSTIGMLRSRLLAHLPKEMTODIEQOLGSLIADDDINQNEFLRLKAKHLN 300	
241 VLENHNRSTIGMLRSRLLAHLPKEMTODIEQOLGSLIADDDINQNEFLRLKAKHLN 300	
QY 301 KDLRLDADDRHMLDIALKADICNPRITWESKOWSERVEEYFROSELROKPLETS 360	
301 KDLRLDADDRHMLDIALKADICNPRITWESKOWSERVEEYFROSELROKPLETS 360	
QY 301 KDLRLDADDRHMLDIALKADICNPRITWESKOWSERVEEYFROSELROKPLETS 360	
301 KDLRLDADDRHMLDIALKADICNPRITWESKOWSERVEEYFROSELROKPLETS 360	
QY 361 PLCNQKDSIPSIQIGMSYIVEPLFERMAHFTGNTLSNNMLGHLAHNAKQKSLPPO 420	

Query Match	23.68;	Score 567.5;	DB 2;	Length 736;
Best Local Similarity	31.38;	Pred. No. 5e-37;		
Matches 129;	Conservative 93;	Mismatches 149;	Indels 41;	Gaps 8;

Query Match 23.5%; Score 565; DB 2; Length 886

Db 318 EQLANE-----LEDTNKGKGLDVEFKVADYSGNRPLTALITFIISFOERDLTKTQIPADTLATYL 374

QY 160 VMVQEDHSQNPYHNAVHADYVTOAMHCYLYKEPKKLASFLLTPIDIMGLLAAAHVDHRC 219

Db 375 LMLEGHYAHANVAHNSHLAAADVAGOSTHYVLTAPRAEAVPTDELTIALPASAHLHDVDDHG 434

QY 220 VNQPLLTNNHLLALXQNSVYLENNHNRSTIGMLRESR--LLAHPRKMTQDIEQOLS 277

Db 435 VSNQGLLTNTSDVALMYNDASVYLENNHLLAVGEKLLQEAENCDFONLSAQRSLSRMVID 494

QY 278 LILATDIRONREFLRKLAHLHNKD-----LRLEDAODRHHMLDIALCADCNCRIM 331

Db 495 MYLATDMSKHNNMLADLTMTVETKATYLSLGVLLDNYSPRIQVLONVLCADISNPTKPL 554

QY 332 EMSKQSERVCEEFYRQGELEQKFELEISPLCNQOKDSIPSTQIGFMSYIVEPPLREMAH 391

Db 555 PLYRQWTRIRIMAEFQOGRERESGLDISPMCDKHNTASVEKSOVGFIDYLAHPLMETWAG 614

QY 392 FTGNSTLENNMGLAHNAKQOKSKLLPRQHR--RGSSSGGGRPH-----DIAGQSTSE 443

Db 615 LVNRP--AQDLDLTLEDNKREYQSKI PRSPSDLTGNPERGDP RPFQELTLEEAEEDEEE 672

QY 444 EOEGD 448

Db 673 EEEGE 677

RESULT 14

167945

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) - rat (fragment)

N:Alternate names: CAMP phosphodiesterase 1

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Nov-2000

C:Accession: I67945, A33904

R:Bolger, G.B.; Rodgers, L.K.; Riggs, M.

Gene 149, 237-244, 1994

A:Title: Differential CNS expression of alternative mRNA isoforms of the mammalian g

A:Reference number: 153865; MUID:95047482

A:Accession: 167945

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-536 <RES>

A:Cross-references: GB:I27061; NID:g436011; PID:NAA56858.1; PID:g436012

R:Swinnen, J.V.; Joseph, D.R.; Concl, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989

A:Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce ca

A:Reference number: A33904; MUID:89315790

A:Accession: A33904

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 230-496 <SMI>

A:Cross-references: GB:M25347; GB:M28410

C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3

C:Keywords: alternative splicing; CAMP binding; phosphoric diester hydrolase

F:235-481/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 22.0%; Score 529.5; DB 2; Length 536;

Best Local Similarity 30.8%; Pred. No. 3,4e-34;

Matches 120; Conservative 79; Mismatches 169; Indels 21; Gaps 7;

QY 71 RLUSQRYFHASRLRGITTPQAPRLHLLDEVDYLGQARHMLSKVGMDFDIFLDRITNGNS 130

Db 156 QITGRKSCHNS-LPTAIAIPRGVOTDDEQLAKE---LEDTNKGKGLDVEFKVAELSGNRP 211

QY 131 LVTLICHLFNNHGLLNHKKLDKMTLHRLVMAQOEYHSQNPRIYHNAVHADYVTOAMHCYLYK 190

Db 212 LTAIVFRLVQERDRLKTFQIPADTLLRLLTLEGGHNSVAAHNSIHADYVQSAHVLLG 271

QY 191 EPKLASFLTPDIDIMGLLAAAHVDHRCVNQPLLTNNHLLALXQNSVYLENNHNRST 250

Db 272 TPRAEAVPTDELTIALPASAHLHDVDDHGVSNQPLNTNSLALMTNDSSVYLENNHLLAVG 331

